

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 8, 2004, 10:53:58 ; Search time 2808 Seconds  
(without alignments)  
5721.458 Million cell updates/sec

Title: US-09-782-745-14

Perfect score: 538

Sequence: 1 AGCCAGGAGCTGTGAGGC.....CTGCAAGAAAAA538

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 28520704

Minimum DB seq length: 0

Maximum DB seq length: 538

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	513	95.4	537	12	BM832793	BM832793 K-EST0107
2	492	91.4	527	12	BI826605	BI826605 603077056
3	491.2	91.3	521	13	EX108227	EX108227 BX108227
4	485.8	90.3	517	14	CF780547	CF780547 AGENCOURT

5	476.8	88.6	509	12	BI868671	BI868671 603392594
6	452.4	84.1	489	9	AA447559	AA447559 zw81e11.s
7	431.4	80.2	457	10	AW510753	AW510753 hd39405.x
8	424.6	78.9	447	9	AI381509	AI381509 te76b07.x
9	424.4	78.9	464	9	AA738037	AA738037 nx15e11.s
10	415.2	77.2	505	14	CB115693	CB115693 K-EST0159
11	413.8	76.9	418	9	AW016546	AW016546 UI-H-B10p
12	413.4	76.8	480	12	BG120336	BG120336 602353732
13	412.8	76.7	426	9	AA868226	AA868226 ak48h07.s
14	410.8	76.4	450	9	AA760996	AA760996 dx32h08.s
15	401.2	74.6	455	9	AI187350	AI187350 qf29a05.x
16	365.4	67.9	412	9	AW102587	AW102587 xd67907.x
17	360.4	67.0	445	11	BC005363	BC005363 Homo sapi
18	359.4	66.8	419	9	AA448542	AA448542 zw81e11.r
19	357	66.4	383	12	BM836228	BM836228 K-EST0111
20	335.2	62.3	341	12	BP431265	BP431265 BP431265
21	329.8	61.3	384	9	AA913206	AA913206 op53f03.s
22	322.4	59.9	383	13	BX283580	BX283580 BX283580
23	318.8	59.3	397	12	BG206349	BG206349 RST25797
24	307.2	57.1	333	13	BUS33718	BUS33718 AGENCOURT
25	296.4	55.1	398	9	AA918604	AA918604 ol53f02.s
26	290.6	54.0	320	12	BM836021	BM836021 K-EST0111
27	269.8	50.1	275	14	CB147043	CB147043 K-EST0202
28	269.8	50.1	275	14	CB150355	CB150355 K-EST0207
29	269.8	50.1	275	14	CB157288	CB157288 K-EST0216
30	253.8	47.2	457	14	CF780497	CF780497 AGENCOURT
31	250.4	46.5	256	12	BG181480	BG181480 RST328 At
32	233.4	43.4	258	12	BG186708	BG186708 RST5683 A
33	228.2	42.4	253	12	BG184057	BG184057 RST2973 A
34	226.6	42.1	261	12	BG199060	BG199060 RST18338
35	224.8	41.8	245	12	BG212621	BG212621 RST32216
36	219.8	40.9	245	12	BG212622	BG212622 RST32217
37	214.8	39.9	292	12	BG208433	BG208433 RST27934
38	213.4	39.7	524	11	AF318372	AF318372 Homo sapi
39	207.6	38.6	507	9	AA972716	AA972716 op90e12.s
40	207	38.5	256	12	BG216461	BG216461 RST36040
41	207	38.5	520	14	CB961487	CB961487 AGENCOURT
42	204.8	38.1	224	9	AA738394	AA738394 nx28c12.s
43	202.4	37.6	382	10	BF869799	BF869799 IL3-ET011
44	200.6	37.3	499	12	BG354572	BG354572 PLAC6 Hum
45	193.8	36.0	197	9	AI968311	AI968311 wd01f07.x

## ALIGNMENTS

RESULT 1  
BM832793  
LOCUS BM832793 537 bp mRNA linear EST 06-MAR-2002  
DEFINITION K-EST0107334 S5SNU484s1 Homo sapiens cDNA clone S5SNU484s1-8-F10  
5', mRNA sequence.  
ACCESSION BM832793  
VERSION BM832793.1 GI:19189202  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 537)  
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.N., Park,H.S., Kim,S. and  
Kim,Y.S.  
TITLE 21C Frontier Korean EST Project 2001  
JOURNAL Unpublished (2002)  
COMMENT Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 8 row: F column: 10  
High quality sequence stop: 537.

## FEATURES

Location/Qualifiers  
1. .537  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="S5SNU484s1-8-F10"  
/sex="M"  
/tissue\_type="Stomach"  
/cell\_type="Epithelial"  
/cell\_line="SNU-484"  
/lab\_host="Top10F"  
/clone\_lib="S5SNU484s1"  
/note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;  
Site 2: NotI. The poly (A)+ RNA was decapped with tabacco  
acid pyrophosphatase (TAP) and ligated with DNA-RNA linker  
including EcoRI site by treatment of T4 RNA ligase. The  
first strand cDNA was synthesized from oligo dr-tailed  
mRNA by priming with dr-tailed vector. The dr-tailed  
vector was adjusted to have about 60nt. The cDNA vector  
was circularized with E. coli DNA ligase after digestion  
of EcoRI which site is also included in vector. An RNA  
strand converted to a DNA strand by Okayama-Berg method.  
The obtained cDNA vectors were used for transformation of  
competent cells E. coli Top10F by electroporation method.  
After analyzing and sequencing about 2,000 ~ 3,000  
colonies in original cDNA library, the abundant cDNAs were  
selected and amplified by PCR reaction using vector region  
primer including T7 promotor as 5' primer and N(dR)14 as  
3' primer. The PCR products were used as template for  
synthesis of biotinylated single stranded RNA by in vitro  
transcription reaction. The synthesized RNA probes were  
hybridized with antisense single stranded cDNAs prepared  
from original library and incubated with avidin-gel.  
After removing DNA-RNA hybrids by centrifuge, the  
subtracted cDNA libraries were constructed by  
transformation of the remaining DNA into competent cells E.  
coli Top10F with electroporation method."

## ORIGIN

Query Match 95.4%; Score 513; DB 12; Length 537;  
Best Local Similarity 98.5%; Pred. No. 3.4e-105;  
Matches 529; Conservative 0; Mismatches 5; Indels 3; Gaps 1;  
QY 3 GCCAGGAGCTGTGAGGAGGCTGTGTTCTCGCGTCGGACTCTTTTCTCTAC 62  
DB 1 GCCAGGAGCTGTGAGGAGGCTGTGTTCTCGCGTCGGACTCTTTTCTCTAC 60  
QY 63 TGAGATTTCATCTGTGAAATATGAGTTGGCGAGGAGATCGAAC---TATCGGCTAGA 119  
DB 61 TGAGATTTCATCTGTGAAATATGAGTTGGCGAGGAGATCGAACCTATTATGGCTAGA 120  
QY 120 CCRAGACCTACGTAGACCTCTGAATGATTTGGGCTATGGCGCTATGGCGGAGCTTCAGT 179  
DB 121 CCAAGGGCTATGTACAGCTCTTGAAGTGTATGGGCTATGGCGCTATGGCGGAGCTTCAGT 180  
QY 180 GATGAAGTGAACACAGCAACCTCAAGAGGGGAAACAGCAACTCAACGTCAGGATCCT 239  
DB 181 GATGAAGTGAACACAGCAACCTCAAGAGGGGAAACAGCAACTCAACGTCAGGATCCT 240  
QY 240 GCAGCTGCTCAGGAGGAGGATGAGGAGATCTGCAGGATCTCAGGCTCAAGGGCCGAGCTGAA 299  
DB 241 GCAGCTGCTCAGGAGGAGGATGAGGAGATCTGCAGGATCTCAGGCTCAAGGGCCGAGCTGAA 300  
QY 300 GCTCATAGCCAGGAGGATGAGGAGATCTGCAGGATCTCAGGCTCAAGGGCCGAGCTGAA 359  
DB 301 GCTCATAGCCAGGAGGATGAGGAGATCTGCAGGATCTCAGGCTCAAGGGCCGAGCTGAA 360  
QY 360 GGGCAGGAGATGGAACCCGCAATCCAGAGGAGGTGAAACCGCTCAAGAGGTTGAAAG 419  
DB 361 GGGCAGGAGATGGAACCCGCAATCCAGAGGAGGTGAAACCGCTCAAGAGGTTGAAAG 420  
QY 420 CAATCACAGTGTAAAAAGACACGTTGAATGATGAGGCTGCTCTATGTTGAAT 479

## Db

421 CAATCACAGTGTAAAAAGAGACAGCTTGAATGATGAGGCTGCTCTATGTTGAAT 480  
QY 480 TTGTTTCATTAATAATCTCCCAATAAAGCTTTTACAGCTTTCTCAAGAAAAA 536  
DB 481 TTGTTTCATTAATAATCTCCCAATAAAGCTTTTACAGCTTTCTCAAGAAAAA 537

## RESULT 2

## BI826605

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## Location/Qualifiers

## 1. .527

## /organism="Homo sapiens"

## /mol\_type="mRNA"

## /db\_xref="taxon:9606"

## /clone="IMAGE:5168892"

## /tissue\_type="medulla"

## /lab\_host="DH10B"

## /clone\_lib="NIH\_MGC\_119"

/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: EcoRV (destroyed); RNA source normal medulla from  
anonymous male age 27. Library is oligo-dr primed and  
directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.3 kb, insert size range  
0.9-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 013. Note:  
this is a NIH\_MGC Library."

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## Conservative

## 0

## Mismatches

## 5

## Indels

## 4

## Gaps

## 2

## QY

## 12

## CTGTGAGGACGTGCTGTGTGTTCTCGCGTCGGAGCTCTTTTCTCTACTGATTC 71

## DB

## 1

## CTGTGAGGACGTGCTGTGTGTTCTCGCGTCGGAGCTCTTTTCTCTACTGATTC 60

## QY

## 72

## TCTGTGTGAATATGAGTTGGCGAGGAGATCGACCTATTATTATGAGGCTTAG 128

## DB

## 61

## TCTGTGTGAATATGAGTTGGCGAGGAGATCGACCTATTATTATGAGGCTTAG 120

## QY

## 129

## TACGTAGAGCTCTGAAATGATGGGCTATGGCGCCGAGGAGCTTCAGTGATCA 188

## DB

## 121

## TATGTACAGCTCTCTGAAATGATGGGCTATGGCGCCGAGGAGCTTCAGTGAT 180

## QY

## 189

## GAACACAGCAACCTGAAAGAGGGGAAACAGCAACTCAACGTCAGGATCCTG 248

## DB

## 181

## GAACACAGCAACCTGAAAGAGGGGAAACAGCAACTCAACGTCAGGATCCTG 240



1. 517  
source

ORGANISM="Homo sapiens"  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:30524555"  
/lab host="DH10B (T1 phage-resistant)"  
/clone lib="NIH\_MGC\_217"  
/note="Vector: pVX-Asc; Site 1: RcoRI; Site 2: NotI; Library is oligo-dT primed and directionally cloned. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with RcoRI adaptor, digested with Not I and then cloned directionally into pVX-Asc vector. Average insert size 0.5-1kb. Adaptors 5' (AATTCGGCAGGAG) 3' and 5'd (CTCGTCCG) 3'. 3' linker sequence - GCGCCGCTCAGAGCC T18. Sequencing primers 3' end: T3 promoter primer 5'd (ATTAACCTCCTCACTAAAGGGA) 3'. 5' End: T7 promoter primer 5'd (TAATACGACTCACTATAGG) 3'. Average insert size 0.5-1kb. Library was constructed in the laboratory of M. Bento Soares. Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 90.3%; Score 485.8; DB 14; Length 517;  
Best Local Similarity 98.1%; Pred. No. 4.5e-99;  
Matches 503; Conservative 0; Mismatches 7; Indels 3; Gaps 1;

14 CTGAGGACGTCGTGTGGTCTCTCCGTCGCGACTCTTTTTCCTCTACTGAGATTCAATC 73  
Db 4 GAGGGCAGTCGTGTGGTCTCTCCGTCGCGACTCTTTTTCCTCTACTGAGATTCAATC 63

74 TGTGTGAATATGAGTTGCGGAGGAGATCGACC---TATCGGCTAGACCAAGACGCTA 130  
Db 64 TGTGTGAATATGAGTTGCGGAGGAGATCGACCTATTATTGGCCCTAGACCAAGCGCTA 123

131 CGTAGAGCTCTCTGAATGATTGGGCTATGCGGCCGAGCAGTTCAGTGAAGTGGGA 190  
Db 124 TGTACAGCTCTCTGAATGATTGGGCTATGCGGCCGAGCAGTTCAGTGAAGTGGGA 183

191 ACCAGCAACACCTGAAAGAGGGGAACCACTCAACGTCAGGATCTCTGAGCTGTCTCA 250  
Db 184 ACCAGCAACACCTGAAAGAGGGGAACCACTCAACGTCAGGATCTCTGAGCTGTCTCA 243

251 GAGGGAGAGGATGAGGAGCATCTCAGGTCAAGGGCCGAGCTGAGCTCATAGCCA 310  
Db 244 GAGGGAGAGGATGAGGAGCATCTCAGGTCAAGGGCCGAGCTGAGCTCATAGCCA 303

311 GGAACGGTTCACCCACAGACTGGGTGTAGTGTGAAGATGTCCTGATGGCCAGGAGAT 370  
Db 304 GGAACGGTTCACCCACAGACTGGGTGTAGTGTGAAGATGTCCTGATGGCCAGGAGAT 363

371 GGACCGCCAAATCCAGAGGAGTGAAAACCGCTGAAGAGGTGAAAACCAATTCAGTGA 430  
Db 364 GGACCGCCAAATCCAGAGGAGTGAAAACCGCTGAAGAGGTGAAAACCAATTCAGTGA 423

431 TTTAAAGACACAGCTTGAATCATGACGCTCTCTCTATCTTGGAAATTTCTTCATTAA 490  
Db 424 TTTAAAGACACAGCTTGAATCATGACGCTCTCTCTATCTTGGAAATTTCTTCATTAA 483

491 AATTCTCCCAATAAAGCTTTTACAGCTTCTTGCA 523  
Db 484 AATTCTCCCAATAAAGCTTTTACAGCTTCTTGCA 516

RESULT 5  
BI868671  
LOCUS 603392594F1 NIH\_MGC\_90 Homo sapiens cDNA clone IMAGE:5402663 5',  
DEFINITION mRNA sequence.  
ACCESSION BI868671  
VERSION BI868671.1 GI:16042344

EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 509)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLNL2026 row: 1 column: 24  
High quality sequence stop: 509.  
Location/Qualifiers  
1. 509  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:5402663"  
/tissue\_type="adenocarcinoma, cell line"  
/lab host="DH10B (phage-resistant)"  
/clone lib="NIH\_MGC\_90"  
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 88.6%; Score 476.8; DB 12; Length 509;  
Best Local Similarity 98.0%; Pred. No. 4.8e-97;  
Matches 494; Conservative 0; Mismatches 7; Indels 3; Gaps 1;

1 ACGCCAGGAGTCGTGAGGACGTCGTGTGGTCTCTCCGTCGCGACTCTTTTTCCTCT 60  
Db 6 ACCTAGGAGTCGTGAGGACGTCGTGTGGTCTCTCCGTCGCGACTCTTTTTCCTCT 65

61 ACTGAGATTCATCTGTGTGAATATGAGTTGCGGAGGAGATCGACC---TATCGGCTTA 117  
Db 66 ACTGAGATTCATCTGTGTGAATATGAGTTGCGGAGGAGATCGACCTATTATTGGCCTA 125

118 GACCAAGACGCTACGTAGAGCTCTCTGAATGATTGGGCTTATGGGCCCCGAGCAGTTCA 177  
Db 126 GACCAAGGCGCTATGACAGCTCTCTGAATGATTGGGCTTATGGGCCCCGAGCAGTTCA 185

178 GTGATGAAGTGAACACCAAGCAACACCTGAAGAGGGGAACCACTCAACGCTCAGGATC 237  
Db 186 GTGATGAAGTGAACCAAGCAACACCTGAAGAGGGGAACCACTCAACGCTCAGGATC 245

238 CTGAGTCGTCTCAGGAGGAGGATGAGGAGCATCTGAGGTCAAGGCCGAGGAGCTG 297  
Db 246 CTGAGTCGTCTCAGGAGGAGGATGAGGAGCATCTGAGGTCAAGGCCGAGGAGCTG 305

298 AAGCTCATAGCCAGGACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGTCGCTG 357  
Db 306 AAGCTCATAGCCAGGACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGTCGCTG 365

358 ATGGGCGAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCTCAGAGAGGTGAAA 417  
Db 366 ATGGGCGAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCTCAGAGAGGTGAAA 425

418 AGCAATCAGCTGTTTAAAGAACACACAGCTTGAATGATGACGCTCTCTCTATGTTGGAA 477  
Db 426 AGCAATCAGCTGTTTAAAGAACACACAGCTTGAATGATGATGATGATGATGATGATGAT 485

478 ATTTGTTTCATTTAAATTTCTCCCA 501



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Db      486 ATTGTTTCATTAATAATCTCCAA 509
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AA447559      489 bp      mRNA      linear      EST 04-JUN-1997
LOCUS      zw81e11.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:782636
DEFINITION      3' similar to TR:G914905 G914905 GAGE-4 PROTEIN. [1] ; mRNA
sequence.
ACCESSION      AA447559
VERSION
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 489)
AUTHORS      Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE      WashU-Merck EST Project 1997
JOURNAL      Unpublished (1997)
COMMENT      Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LInL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m3 fwd. ET from Amersham
High quality sequence stop: 427.
FEATURES
Location/Qualifiers
1..489
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:782636"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis NHT"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
Primer [5]
TGTTACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTT 3'.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN
Query Match      84.1%; Score 452.4; DB 9; Length 489;
Best Local Similarity 98.0%; Pred. No. 1.5e-91;
Matches 480; Conservative 0; Mismatches 6; Indels 4; Gaps 2;
QY      43 CGGACTCTTTTCTCTACTGAGATTCATCTGTGTAATATGTTGGCGAGGAAGAT 102
Db      489 CGGACTCTTTTCTCTACTGAGATTCATCTGTGTAATATGTTGGCGAGGAAGAT 430
QY      103 CGACC---TATCGGCTAGACCAAGACGCTAGTAGCCCTCTGAAATGATTTGGGCTTA 159
Db      429 CGACTATATTGGCTTAGACCAAGGCGCTATGTACAGCCCTCTCTGAATGATT-GGGCTA 371
QY      160 TGGCGCCCGCAGCTTCAGTGATGAAGTGGACCAAGCAACACCTGAAGAGGGAACCG 219
Db      370 TGGCGCCCGCAGCTTCAGTGATGAAGTGGACCAAGCAACACCTGAAGAGGGAACCG 311
QY      220 CAATCTCAACGTCAGGATCTCTGAGCTGTCTAGGAGGAGGAGGATGAGGAGCATCTGCAG 279

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Db      310 CAACTCAACGTCAGGATCTCTGCAGCTGCTCAGGAGGAGAGGATGAGGGAGCATCTGCAG 251
QY      280 GTCAAGGGCCGAAGCCCTGAAGCTCATAGCCAGGAACAGGGTCAACCCACAGACTGGGTGTG 339
Db      250 GTCAAGGGCCGAAGCCCTGAAGCTCATAGCCAGGAACAGGGTCAACCCACAGACTGGGTGTG 191
QY      340 AGTGTGAAGATGCTCTCTGATGGGCGAGAGATGGACCCGCAAAATCCAGAGGAGGTGAAA 399
Db      190 AGTGTGAAGATGCTCTCTGATGGGCGAGAGATGGACCCGCAAAATCCAGAGGAGGTGAAA 131
QY      400 CGCCTCAAGAAGGTGAAAAGCAATCAAGTTPAAAAGAGACACACGTTGAAATGATGCAG 459
Db      130 CGCCTCAAGAAGGTGAAAAGCAATCAAGTTPAAAAGAGGCACTTGAAATGATGCAG 71
QY      460 GCTGCTCTCTATGTTGAAAATTTGTCATTAATAATCTCCCAATAAGCTTTACAGCTTTC 519
Db      70 GCTGCTCTCTATGTTGAAAATTTGTCATTAATAATCTCCCAATAAGCTTTACAGCTTTC 11
QY      520 TGCAAAGAAA 529
Db      10 TGCAAAGAAA 1
RESULT 7
AWS10753/c
LOCUS
DEFINITION      AWS10753.1 457 bp      mRNA      linear      EST 03-MAR-2000
hd39d05.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
IMAGE:2911881 3' similar to SW:GGE4_HUMAN Q13069 GAGE-4 PROTEIN. ;,
mRNA sequence.
ACCESSION      AWS10753
VERSION      AWS10753.1 GI:7148831
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 457)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LInL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40JP from Gibco.
FEATURES
Location/Qualifiers
1..457
/organism="Homo sapiens"
/mol_type="mRNA"
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/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI CGAP-GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
724808-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
ORIGIN
Query Match      80.2%; Score 431.4; DB 10; Length 457;
Best Local Similarity 98.0%; Pred. No. 8.2e-87;
Matches 448; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

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77 GTGAATATGAGTTGGCGAGGAGATCGACCTATC---GGCCTAGACCAAGAGCGTACCT 133  
 457 GTGAATATGAGTTGGCGAGGAGATCGACCTATC---GGCCTAGACCAAGGCGCTATGT 398  
 134 AGAGCCTCTGAAATGATTGGGCTATGGGCGGAGCAGTTCAGTGAATGGAAC 193  
 397 ACGCCTCTGAAATGATTGGGCTATGGGCGGAGCAGTTCAGTGAATGGAAC 338  
 194 AGCAACACCTGAAAGAGGGAACCAAGCAATCAAGTCAAGATCCTGAGCTCTCAGGA 253  
 337 AGCAACACCTGAAAGAGGGAACCAAGCAATCAAGTCAAGATCCTGAGCTCTCAGGA 278  
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 277 GGGAGAGGATGAGGAGGAGATCTCAGTCAAGGCGGAGCCTGAAGCTCATAGCCAGGA 218  
 314 ACAGGCTCACCAAGAGGAGATCTCAGTCAAGGCGGAGCCTGAAGCTCATAGCCAGGA 373  
 217 ACAGGCTCACCAAGAGGAGATCTCAGTCAAGGCGGAGCCTGAAGCTCATAGCCAGGA 158  
 374 CCGCCCAATCCAGAGGAGTGAAGAGCCTGAAGAGGTTGAAGCAATCAAGTGTGA 433  
 157 CCGCCCAATCCAGAGGAGTGAAGAGCCTGAAGAGGTTGAAGCAATCAAGTGTGA 98  
 434 AAGAGACAGCTTGAATGATGAGGCTGCTCTATGTTGGAATTTGTTCAATAAAT 493  
 97 AAGAGAGGAGCTTGAATGATGAGGCTGCTCTATGTTGGAATTTGTTCAATAAAT 38  
 494 TCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA 530  
 37 TCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA 1

RESULT 8  
 AI381509/c  
 LOCUS  
 DEFINITION te76b07.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone  
 IMAGE:2092597 3' Similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;  
 mRNA sequence.  
 AI381509  
 AI381509.1 GI:4194290  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 447)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
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 a modified polylinker; Site 1: Not 1; Site 2: Eco RI;  
 Equal amounts of plasmid DNA from three normalized  
 libraries (fetal lung Nhlh19w, testis NHT, and B-cell  
 NCI-CGAP\_GCB1) were mixed, and ss circles were made in  
 vitro. Following HAP purification, this DNA was used as  
 tracer in a subtractive hybridization reaction. The driver  
 was PCR-amplified cDNAs from pools of 5,000 clones made

from the same 3 libraries. The pools consisted of  
 I.M.A.G.E. clones 297480-302087, 682632-687239,  
 726408-728711, and 729096-731399. Subtraction by Bento  
 Soares and M. Fatima Bonaldo. "

ORIGIN  
 Query Match 78.9%; Score 424.6; DB 9; Length 447;  
 Best Local Similarity 98.4%; Pred. NO. 2.8e-85;  
 Matches 440; Conservative 0; Mismatches 4; Indels 3; Gaps 1;  
 QY 88 GTTGGCAGGAGATCGAC---TATCGGCTAGACCAAGAGCCTACGTAGAGCTCCTG 144  
 DB 447 GTTGGCAGGAGATCGACCTATTATTGGCTAGACCAAGGCGCTATGTATACGCTCCTG 388  
 QY 145 AAATGATTGGGCTATCGGCGGAGCAGTTCAGTGAATGGAACCAAGCAACCTG 204  
 DB 387 AAATGATTGGGCTATCGGCGGAGCAGTTCAGTGAATGGAACCAAGCAACCTG 328  
 QY 205 AAGAAGGGGAACAGCAACTCAACGTCAGGATCCTGAGCTGCTCAGGAGGAGAGGATG 264  
 DB 327 AAGAAGGGGAACAGCAACTCAACGTCAGGATCCTGAGCTGCTCAGGAGGAGAGGATG 269  
 QY 265 AGGAGCATCTGAGGTCGAAGGCGGAGCCTGAAGCTCATAGCCAGGAACAGGCTCACC 324  
 DB 267 AGGAGCATCTGAGGTCGAAGGCGGAGCCTGAAGCTCATAGCCAGGAACAGGCTCACC 208  
 QY 325 CACAGACTGGTGTGAGTGTGAAGATGGTCTGATGGCGAGGAGATGGAACCGCAATC 384  
 DB 207 CACAGACTGGTGTGAGTGTGAAGATGGTCTGATGGCGAGGAGATGGAACCGCAATC 148  
 QY 385 CAGAGGAGGTGAAAAAGCCTGAAGAGGTGAAGCAATCACAGTGTAAAAAGAGACAC 444  
 DB 147 CAGAGGAGGTGAAAAAGCCTGAAGAGGTGAAGCAATCACAGTGTAAAAAGAGACAC 88  
 QY 445 GTTCATATGATGAGGCTGCTCTATGTTGGAATTTGTTCAATAAATTTCTCCCAATAA 504  
 DB 87 GTTCATATGATGAGGCTGCTCTATGTTGGAATTTGTTCAATAAATTTCTCCCAATAA 28  
 QY 505 AGCTTTACAGCCTTCTGCAAGAAAAA 531  
 DB 27 AGCTTTACAGCCTTCTGCAAGAAAAA 1

RESULT 9  
 AA738037/c  
 LOCUS  
 DEFINITION nx15ell.s1 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1256204 3'  
 similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ; mRNA sequence.  
 ACCESSION AA738037  
 VERSION AA738037.1 GI:2768794  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 464)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html  
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FEATURES  
source

Location/Qualifiers  
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/note="Vector: pTV73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - Cligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTV73 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 78.9%; Score 424.4; DB 9; Length 464;  
Best Local Similarity 96.9%; Pred. No. 3.1e-85;  
Matches 444; Conservative 0; Mismatches 11; Indels 3; Gaps 1;  
QY 84 ATGAGTTGGCGAGGAAGATCGACCTTTATGGCCCTAGACCAAGACGGCTACCTAGAGCCT 140  
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QY 141 COTGAATGATTGGCCCTATCGGCCCGAGCAGTTCAGTGATGAAGTGAACCAACCAACA 200  
DB 404 COTGAATGATTGGCCCTATCGGCCCGAGCAGTTCAGTGATGAAGTGAACCAACCAACA 345  
QY 201 COTGAAGAGGGGAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 260  
DB 344 COTGAAGAGGGGAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 285  
QY 261 GATGAGGAGCATCGCAGGTCAAGGCCGGAAGCCTGAAGCTCATAGCAGGAAACAGGGT 320  
DB 284 GATGAGGAGCATCGCAGGTCAAGGCCGGAAGCCTGAAGCTCATAGCAGGAAACAGGGT 225  
QY 321 CACCCACAGCTGGGTGAGTGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAG 380  
DB 224 CACCCACAGCTGGGTGAGTGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAG 165  
QY 381 AATCCAGAGGAGTGAAGAACCGCTCAAGAGTGAAGAACCAATCAACAGTGTAAAGAG 440  
DB 164 AATCCAGAGGAGTGAAGAACCGCTCAAGAGTGAAGAACCAATCAACAGTGTAAAGAG 105  
QY 441 ACAGTTGAATGATGACGGTGTCTTATGTTGAAATTTGTTCAATTAATTTCTCCCA 500  
DB 104 GCAGCTTGAATGATGACGGTGTCTTATGTTGAAATTTGTTCAATTAATTTCTCCCA 45  
QY 501 ATAAGCTTTACAGCTTCTCCAAAGAAAAA 538  
DB 44 ATAAGCTTTACAGCTTCTCCAAAGAAAAA 7

RESULT 10  
CB115693  
LOCUS  
DEFINITION X-EST0159805 L8SCK0 Homo sapiens cDNA clone L8SCK0-8-B09 5', mRNA  
sequence.  
ACCESSION CB115693  
VERSION CB115693.1 GI:27941500  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 505)  
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.  
TITLE 21C Frontier Korean EST Project 2001

JOURNAL  
COMMENT

Unpublished (2002)  
Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 8 row: B column: 09  
High quality sequence stop: 505.

## FEATURES

source  
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/note="Organ: Liver; Vector: pTV73-Pac; Site 1: EcoRI; Site 2: NotI; The library was constructed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cell culture."

## ORIGIN

Query Match 77.2%; Score 415.2; DB 14; Length 505;  
Best Local Similarity 96.5%; Pred. No. 3.7e-83;  
Matches 436; Conservative 0; Mismatches 13; Indels 3; Gaps 1;  
QY 32 GTTCTGCGCTCGGACACTCTTTTCTCTACTGAGATTCATCTGTGTAATATGAGTTG 91  
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QY 92 GCGAGGAGATCGACC---TATCGGCTAGACCAAGACGCTACGTAGAGCTCTCTGAAT 148  
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QY 149 GATTGGGCTATGCGCCGAGCAGTTCAGTGATCAAGTGAACCAACCAACCAACCAACCA 208  
DB 139 GATTGGGCTATGCGCCGAGCAGTTCAGTGATCAAGTGAACCAACCAACCAACCAACCA 198  
QY 209 AGGGGAACCAAGCAACTCAACGTCAAGTCTCTGAGCTGCTCAGGAGGAGAGTGAAGG 268  
DB 199 AGGGGAACCAAGCAACTCAACGTCAAGTCTCTGAGCTGCTCAGGAGGAGAGTGAAGG 258  
QY 269 AGCATCTGAGGTCAAGGCCGGAAGCCTGAAGCTCTAGCCAGGAAACAGGGTCAACCA 328  
DB 259 AGCATCTGAGGTCAAGGCCGGAAGCCTGAAGCTCTAGCCAGGAAACAGGGTCAACCA 318  
QY 329 GACTGGGTGTGAGTGTCAGATGCTGATGGCAGAGATGACCGCCCAATCCAGA 388  
DB 319 GACTGGGTGTGAGTGTCAGATGCTGATGGCAGAGATGACCGCCCAATCCAGA 378  
QY 389 GGAGGTGAAAACCGCTCAAGAGGTGAAAAGCAATCAAGTGTAAAGAGACACCTTG 448  
DB 379 GGAGGTGAAAACCGCTCAAGAGGTGAAAAGCAATCAAGTGTAAAGAGACACCTTG 438  
QY 449 AATGATGACGGTGTCTCTATGTTGAAAT 480  
DB 439 AATGATGACGGTGTCTCTATGTTGAAAT 470

RESULT 11  
AW016546/c  
LOCUS  
DEFINITION UI-H-B10p-abg-g-06-0-UI.s1 NCI CGAP\_Sub2 Homo sapiens cDNA clone  
IMAGE:2711986 3', mRNA sequence.  
ACCESSION AW016546  
VERSION AW016546.1 GI:5865303  
KEYWORDS EST.

AW016546 418 bp mRNA linear EST 10-SEP-1999  
UI-H-B10p-abg-g-06-0-UI.s1 NCI CGAP\_Sub2 Homo sapiens cDNA clone  
IMAGE:2711986 3', mRNA sequence.





DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 331.  
Location/Qualifiers

FEATURES

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polylinker; 1st strand cDNA was prepared from 3 pooled  
germ cell tumors, and was then primed with a Not I -  
oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified p7T3  
vector. Library is normalized. Library was constructed by  
Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 76.4%; Score 410.8; DB 9; Length 450;  
Best Local Similarity 97.3%; Pred. No. 3.6e-82; Indels 4; Gaps 2;  
Matches 439; Conservative 0; Mismatches 8;  
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Db 390 COTGAATGANTGTGCCTATGCGGCCGAGCAGTTTCAGTGATGAAGTGAACCAAGCAACA 331  
QY 201 COTGAAGAGGGAACCAAGCAACTCAAGTCAGGATCTGAGCTGCTCAGGAGGAGAG 260  
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QY 261 GATGAGGAGCAGCATCTGAGGTCAAGGCGCGAAGCTCAAGCTCATAGCCAGGAACAGGGT 320  
Db 270 GATGAGGAGCAGCATCTGAGGTCAAGGCGCGAAGCTCAAGCTCATAGCCAGGAACAGGGT 211  
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Db 210 CACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGATGGCAGGAGATGACCCGCCA 151  
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Db 150 AATCCAGAGGAGTGAACACGCTGAGAAGCTGAAAAGCAATCAGTGTAAAGAGAG 91  
QY 441 ACACGTTGAATGATGACGGCTGCTCTATGTTGAAATTTGTTCAATTAATTTCTCCCA 500  
Db 90 ACACGTTGAATGATGACGGCTGCTCTATGTTGAAATTTGTTCAATTAATTTCTCCCA 31  
QY 501 ATAAAGCTTTACAGCTTTCGAAGAAAAA 531  
Db 30 ATAAAG-TTACAGCTTTCGAAGAAAAA 1

RESULT 15

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DEFINITION  
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sequence.  
ACCESSION  
AI187350  
VERSION  
AI187350.1  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 455)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-i@mail.nih.gov  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
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Seq primer: -40UP from Gibco  
High quality sequence stop: 391.  
Location/Qualifiers

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES

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was prepared from mRNA obtained from Clontech  
Laboratories, Inc., and primed with a Not I - oligo(dT)  
primer [5].  
TGTACCAATCTGAAGTGGGCGCGCCCAATTTTTTTTTTTT 3'.  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified p7T3 vector. Library  
went through one round of normalization to Cots, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 74.6%; Score 401.2; DB 9; Length 455;  
Best Local Similarity 95.4%; Pred. No. 5.2e-80; Indels 3; Gaps 2;  
Matches 435; Conservative 0; Mismatches 18;  
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Db 455 ATGAGTTGGCGAGGAAGATGACCTATTATTGGCTAGACCAAGCGCTATGT-CAGCCTC 397  
QY 142 CTGAATGATTTGGGCTATGCGGCCGAGCAGTTTCAGTGATGAAGTGAACCAAGCAACAC 201  
Db 396 CTGAATGATTTGGGCTATGCGGCCGAGCAGTTTCAGTGATGAAGTGAACCAAGCAACAC 337  
QY 202 CTGAAGAGGGGAACCAAGCACTCAACGTGAGATCTTCGAGTCTCAGGAGGAGAGG 261  
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QY 262 ATGAGGAGCATCTCAGGTCAAGGCGCAAGCCCTGAAGCTCATGCCAGGAACAGGGTTC 321  
Db 276 ATGAGGAGCATCTCAGGTCAAGGCGCAAGCCCTGAAGCTCATGCCAGGAACAGGGTTC 217  
QY 322 ACCCAGAGCTGGGTGTGAGTGTGAAGATGGTCTTGATGGGAGGAGATGGACCCGCA 381  
Db 216 ACCCAGAGCTGGGTGTGAGTGTGAAGATGGTCTTGATGGGAGGAGATGGACCCGCA 157  
QY 382 ATCCAGAGCAGTGAAGAACGCTGAAAGAGGTGAAAAGCAATCACAGTGTAAAAAGAGA 441  
Db 156 ATCCAGAGCAGTGAAGAACGCTGAAAGAGGTGAAAAGCAATCACAGTGTAAAAAGAGA 97  
QY 442 CACGTTGAATGATGAGGCTGCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCA 501  
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Job time : 2817 secs



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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
6143.899 Million cell updates/sec

Title: US-09-782-745-14

Perfect score: 538

Sequence: 1 ACGCCAGGAGCTGTGAGGC.....CTGCAAGAGAAAAA 538

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 5017792

Minimum DB seq length: 0

Maximum DB seq length: 538

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002s:\*

7: geneseqn2003as:\*

8: geneseqn2003bs:\*

9: geneseqn2003cs:\*

10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	538	100.0	538	2 AAX90519	GAGE-2 tu
2	530	98.5	530	7 ABZ20463	GAGE-2 fu
3	525.4	97.7	528	7 ADAL5801	Human GAG
4	504.8	93.8	532	2 AAX90522	GAGE-5 tu
5	501.4	93.2	528	6 ABZ166323	Lung canc
6	498.8	92.7	527	7 ACC51027	Human bla
7	498.8	92.7	527	7 ABX76236	Lung canc
8	496.8	92.3	532	2 AAV18720	cdna enco
9	493	91.6	535	2 AAV18717	cdna enco
10	488	90.7	526	7 ADAL5802	Human GAG
11	357.8	66.5	430	3 AAC02129	Human sec
12	301.4	56.0	530	4 AAS60104	Human can
13	299.2	55.6	365	4 AAS60496	Human can
14	241.4	44.9	259	7 ABZ19791	Group III
15	225	41.8	225	7 ABZ19533	Group III
16	223.6	41.6	257	7 ABZ19955	Group III
17	223.6	41.6	264	7 ABZ19755	Group III
18	222	41.3	277	7 ABZ19551	Group III
19	216.6	40.3	520	7 ABT15737	Human can
20	209	38.8	509	7 ABX77605	Different
21	209	38.8	509	8 ACB42232	Human GAG
22	209	38.8	509	9 ADC24646	Human cDN
23	206.6	38.4	229	7 ABZ20497	TPS1 subt

C	24	203	37.7	227	7	ABZ20480	TPS1 subt
c	25	202	37.5	229	7	ABZ18686	Group III
	26	201	37.4	219	7	ABZ19538	Group III
	27	194	36.1	532	4	AAI60530	Human pol
	28	172.4	32.0	503	5	AAS69484	DNA enco
	29	153	28.4	528	7	ABT15728	Human can
	30	130.4	24.2	475	4	ADL14981	Human can
	31	125.4	23.3	538	7	ABT15736	Human NOV
	32	108	20.1	399	5	AAF68151	Human can
	33	108	20.1	399	6	ABK38062	cdna enco
	34	108	20.1	399	7	ACA10391	Human can
	35	108	20.1	399	7	ABX99342	Lung canc
	36	108	20.1	399	10	ADE72125	Human dif
	37	103.6	19.3	505	6	ADZ42228	Human dif
	38	103.4	19.2	463	6	ABA92217	Melanoma
	39	101.6	18.9	515	4	AAH93807	Human pro
	40	101.6	18.9	515	4	AAS63900	Human pro
	41	101.6	18.9	515	4	AAH02872	Prostate
	42	101.6	18.9	515	4	AAH85121	Human pro
	43	101.6	18.9	515	5	ACA59708	Prostate
	44	101.6	18.9	515	6	ABJ95271	Human P10
	45	101.6	18.9	515	7	ACC95435	Prostate

## ALIGNMENTS

## RESULT 1

AAX90519

ID AAX90519 standard; cDNA; 538 BP.

AC AAX90519;

XX

DT 30-SEP-1999 (first entry)

XX

GAGE-2 tumour rejection antigen clone nucleotide sequence.

Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection; therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte; GAGE; ss.

XX Homo sapiens.

OS

XX

PN WO9937665-A1.

XX

PD 29-JUL-1999.

XX

PF 12-JAN-1999; 99WO-US000775.

XX

PR 23-JAN-1998; 98US-00012818.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Falleur T;

XX WPI; 1999-469111/39.

DR

XX

PT

PT

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

XX

SQ

Sequence 538 BP; 160 A; 116 C; 155 G; 107 T; 0 U; 0 Other;





1	AGCTGTGAGGCAGTGCCTGTGTGGTTCCTGCCGTCCGGACTCTTTTTCCTCTACTAGATT	60
70	CATCTGTGTGAATAATGATGATTGGCGAGGAAGATCGACC--TATCGGCTGACCAAGAC	126
61	CATCTGTGTGAATATGATGATTGGCGAGGAAGATCGACCTATTTATTTGGCTTAGCAAGGC	120
127	GCTACGTAGAGCCTCCTGAATGATTTGGGCCCTATTCGGCCCGAGCAGTTTCAGTGATGAAG	186
121	GCTATGTCACGCTCCTGAACTGATTGGSCCTATCGCGCCCGAGCAGTTTCAGTGATGAAG	180
187	TGGAACACAGCAACCTGAAAGAGGGGAAACAGCGAACTCAAGTCAGATCAGATCCTGAGCTG	246
181	TGGAACACAGCAACCACTGAAGAAGGGGAACCAAGCAACTCAACGTGAGGATCCTGAGCTG	240
247	CTCAGGAGGGAGAGATCAGAGGAGCATCTGCAGGTCAAGGGCCGAAGCTGGAAGCTCAT	306
241	CTCAGGAGGGAGAGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCTGGAAGCTGATA	300
307	GCCAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGTGATGGCGAG	366
301	GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGTGATGGCGAG	360
367	AGATGHCACCGCCAAATCCAGAGGAGGTGAAAACGCCCTGAAAGAGGTGAAAAGCAATCAC	426
361	AGATGGAACCGGCCAAATCCAGAGGAGGTGAAAACGCCCTGAAAGAGGTGAAAAGCAATCAC	420
427	AGTGTTTAAAGAAGACAGTTGAAATGATGCAAGGTGCTCCTATGTGTGAAAATTTGTTTCA	486
421	AGTGTTTAAAGAAGACAGTTGAAATGATGCAAGGTGCTCCTATGTGTGAAAATTTGTTTCA	480
487	TTAAATTTCTCCATAAAGCTTTTACGCTTCTGCAAGAAAAA	538
481	TTAAATTTCTCCATAAAGCTTTACGCTTCTGCAAGAAAAA	532

DEPT. OF

[illegible]

```
QY 119 ACCAAGCAGCTAGTAGAGCTCTCTGAAATGATTGGCCCTATCGCGCCCGAGCAGTTCCAG 178
D 121 ACCAAGCGCTATGTACAGCTCTCTGAAATGATTGGCCCTATCGCGCCCGAGCAGTTCCAG 180
QY 179 TGATGAAGTGGACCAACCAACACCTCTGAAGAGGGGAACCAAGCAACTCAACGTCAGGATCC 238
D 181 TGATGAAGTGGACCAACCAACACCTCTGAAGAGGGGAACCAAGCAACTCAACGTCAGGATCC 240
QY 239 TGCAGTGTCTCAGGAGGAGAGGATGAGGAGCATCTGCAGGTCAAGGCCGGAAGCTCGA 298
D 241 TGCAGTGTCTCAGGAGGAGAGGATGAGGAGCATCTGCAGGTCAAGGCCGGAAGCTCGA 300
QY 299 ACCTCATGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAGATGGTCTTCA 358
D 301 ACCTCATGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAGATGGTCTTCA 360
QY 359 TGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAGAGCCCTGAAGAAAGGTGAAA 418
D 361 TGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAGAGCCCTGAAGAAAGGTGAAA 420
QY 419 GCAATCACAGTGTAAAGAGACACAGCTTGAATGATGAGGCTGCTCTTATGTTGAAA 478
D 421 GCAATCACAGTGTAAAGAGACACAGCTTGAATGATGAGGCTGCTCTTATGTTGAAA 480
QY 479 TTGTTTCATTAATAATCTCCCAATAAAGCTTTTACAGCCTTCTGCAA 525
D 481 TTGTTTCATTAATAATCTCCCAATAAAGCTTTTACAGCCTTCTGCAA 527

RESULT 6
ACC51027
ID ACC51027 standard; cDNA; 527 BP.
XX
AC ACC51027;
XX
DT 12-JUN-2003 (first entry)
XX
DE Human bladder cancer associated cDNA sequence SEQ ID NO:144.
XX
XX Human; bladder cancer; cytostatic; gene therapy; vaccine; gene; ss.
OS Homo sapiens.
EN WO2003003906-A2.
XX
PD 16-JAN-2003.
XX
PF 03-JUL-2002; 2002WO-US021338.
XX
PR 03-JUL-2001; 2001US-0302814P.
PR 03-AUG-2001; 2001US-0310099P.
PR 08-NOV-2001; 2001US-0343705P.
PR 13-NOV-2001; 2001US-0350666P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Mack DH, Aziz N;
PI
XX WPI; 2003-201532/19.
XX
DR P-PSDB; ABR48213.
XX
PT Detecting a bladder cancer-associated transcript in a cell from a
PT patient, comprises contacting a biological sample from the patient with a
PT bladder cancer-associated polynucleotide or antibody.
XX
PS Claim 6; Page 279; 307pp; English.
XX
CC The present invention describes a method for detecting a bladder cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with a polynucleotide
CC that selectively hybridises to a sequence that is 80 % identical to a
```

```
CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
CC encode the human bladder cancer-associated proteins given in ABR48146 to
CC ABR48242). Bladder cancer-associated sequences from the present invention
CC have cytostatic activities, and can be used in antisense gene therapy and
CC in vaccine production. The method can be used for detecting a bladder
CC cancer-associated transcript in a cell from a patient. The method is
CC useful in diagnosing or treating bladder cancer and in screening for
CC compounds that modulate bladder cancer, such as hormones or antibodies.
CC The nucleic acid molecules from the present invention may be used in
CC various screening and diagnostic methods, and for gene therapy, vaccine
CC and/or antisense/inhibition applications
XX
SQ Sequence 527 BP; 146 A; 113 C; 157 G; 111 T; 0 U; 0 Other;
Query Match 92.7%; Score 498.8; DB 7; Length 527;
Best Local Similarity 98.1%; Pred. No. 1.5e-134;
Matches 516; Conservative 0; Mismatches 7; Indels 3; Gaps 1;
QY 3 GCCAGGAGCTGTGAGGAGTGTCTGTGGTCTCTGCTCGGCTCGGACTCTTTTCTCTAC 62
D 1 GCCAGGAGCTGTGAGGAGTGTCTGTGGTCTCTGCTCGGCTCGGACTCTTTTCTCTAC 60
QY 63 TGAGATTTCATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACC---TATCGGCTAGA 119
D 61 TGAGATTTCATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTAGA 120
QY 120 CCAAGACGCTACGTAGAGCTCTCTGAATGATTTGGGCTTATCGGCGCCGAGCAGTTCA 179
D 121 CCAAGCGCTATGTACAGCTCTCTGAAGTGAATTGGGCTTATCGGCGCCGAGCAGTTCA 180
QY 180 GATGAAGTGGACCAACCAACCTCTGAAGAGGGGAACCAAGCAACTCAACGTCAGATCCT 239
D 181 GATGAAGTGGACCAACCAACCTCTGAAGAGGGGAACCAAGCAACTCAACGTCAGATCCT 240
QY 240 GCAGCTGTCTCAGGAGGAGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAGCTGAA 299
D 241 GCAGCTGTCTCAGGAGGAGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAGCTGAA 300
QY 300 GCTCATAGCCAGGAACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGAT 359
D 301 GCTCATAGCCAGGAACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGAT 360
QY 360 GGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAGAGCCCTGAAGAAAGTGA 419
D 361 GGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAGAGCCCTGAAGAAAGTGA 420
QY 420 CAATCACAGTGTTAAGAGAGACACGTTTGAATGATGAGGCTGCTCTTATGTTGAAAT 479
D 421 CAATCACAGTGTTAAGAGAGACACGTTTGAATGATGAGGCTGCTCTTATGTTGAAAT 480
QY 480 TTGTTTCATTAATAATCTCCCAATAAAGCTTTTACAGCCTTCTGCAA 525
D 481 TTGTTTCATTAATAATCTCCCAATAAAGCTTTTACAGCCTTCTGCAA 526

RESULT 7
ABX76236
ID ABX76236 standard; DNA; 527 BP.
XX
AC ABX76236;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polynucleotide #105.
XX
DE Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
XX antiinflammatory; antisthmatic; non-small cell lung cancer; atelectasis;
XX small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
XX chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
XX interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
```

PN WO200286443-A2.  
 XX 31-OCT-2002.  
 XX 18-APR-2002; 2002WO-US012476.  
 XX 18-APR-2001; 2001US-0284770P.  
 PR 10-MAY-2001; 2001US-0250492P.  
 PR 09-NOV-2001; 2001US-0339245P.  
 PR 13-NOV-2001; 2001US-0350666P.  
 PR 29-NOV-2001; 2001US-0334370P.  
 PR 12-APR-2002; 2002US-0372246P.  
 XX (BOSB-) BOS BIOTECHNOLOGY INC.  
 XX Aziz N, Murray R;  
 XX WPI; 2003-093161/08.  
 DR P-PSDB; ABUS6512.  
 XX  
 PT Detecting a lung cancer-associated transcript in a cell from a patient  
 PT for treating lung cancer, by contacting a biological sample from the  
 PT patient with a polynucleotide that exhibits increased or decreased  
 PT expression in lung cancer.  
 XX  
 PS Claim 22; Page 273; 453pp; English.  
 XX  
 CC The invention relates to a method for detecting a lung cancer-associated  
 CC transcript in a cell from a patient, comprising contacting a biological  
 CC sample from the patient with a polynucleotide that selectively hybridises  
 CC to a sequence that is at least 80 % identical to a gene that exhibits  
 CC increased or decreased expression in lung cancer samples. Lung cancer-  
 CC associated polynucleotides and polypeptides are used for identifying a  
 CC compound that modulates a lung cancer-associated polypeptide, for  
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung  
 CC cancer in a patient and for treating a mammal having lung cancer by  
 CC administering a modulatory compound identified. The methods are useful  
 CC for treating lung cancer, such as small cell lung cancer, non-small cell  
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,  
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,  
 CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and  
 CC bronchiectasis. The genes, polynucleotides and polypeptides are useful  
 CC for diagnostic purposes and as targets for screening for therapeutic  
 CC compounds that modulate lung cancer, such as antibodies. Sequences  
 CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the  
 CC invention  
 XX  
 SQ Sequence 527 BP; 146 A; 113 C; 157 G; 111 T; 0 U; 0 Other;  
 Query Match 92.7%; Score 498.8; DB 7; Length 527;  
 Best Local Similarity 98.1%; Pred. No. 1.5e-134;  
 Matches 516; Conservative 0; Mismatches 7; Indels 3; Gaps 1;  
 3 GCCAGGAGCTGTGAGGAGTGTGTGTGTCTGCGGTCGGGACCTTTTCTCTAC 62  
 1 GCCAGGAGCTGTGAGGAGTGTGTGTGTCTGCGGTCGGGACCTTTTCTCTAC 60  
 63 TGAGATTCATCTGTGTAATATGATGTTGGGAGGAGATCGACC---TATCGGCTAGA 119  
 61 TGAGATTCATCTGTGTAATATGATGTTGGGAGGAGATCGACCTATTATGGCCCTAGA 120  
 120 CCAAGAGCTACGTAGAGCTTCTGTAATGATTTGGGCTATGCGGCCCGAGCAGTTCAGT 179  
 121 CCAAGGCGCTATGTACAGCTTCTGTAATGATTTGGGCTATGCGGCCCGAGCAGTTCAGT 180  
 180 GATGAAGTGAACACGACGACCTGAAAGGGGACAGCAACTCAACGTACAGTTCCT 239  
 181 GATGAAGTGAACACGACGACCTGAAAGGGGACAGCAACTCAACGTACAGTTCCT 240  
 240 GCAGTGTCTAGGAGGAGAGGATGAGGAGCATCTGAGGTCAAGGGCCGAGCCTGAA 299  
 241 GCAGTGTCTAGGAGGAGAGGATGAGGAGCATCTGAGGTCAAGGGCCGAGCCTGAA 300

QY 300 GCTCATAGCCAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGAT 359  
 DB |||||  
 QY 301 GCTGATAGCCAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGAT 360  
 DB |||||  
 QY 360 GGGCAGGAGATGACCCGCCCAAAATCCAGAGGAGGTGAAAACGGCTGAGAAAGTGAAG 419  
 DB |||||  
 QY 361 GGGCAGGAGGTGACCCGCCCAAAATCCAGAGGAGGTGAAAACGGCTGAGAAAGTGAAG 420  
 DB |||||  
 QY 420 CAATCAAGTGTAAAGAGAGACAGCTTGAATGATGATGATGATGATGATGATGATGATGAT 479  
 DB |||||  
 QY 421 CAATCAAGTGTAAAGAGAGACAGCTTGAATGATGATGATGATGATGATGATGATGATGAT 480  
 DB |||||  
 QY 480 TTGTTTCATTAATAATTTCTCCCAATAAAGCTTTTACAGCCCTTCTGCAAA 525  
 DB |||||  
 QY 481 TTGTTTCATTAATAATTTCTCCCAATAAAGCTTTTACAGCCCTTCTGCAAA 526  
 DB |||||  
 RESULT 8  
 AAV18720  
 ID AAV18720 standard; cDNA; 532 BP.  
 XX  
 AC AAV18720;  
 XX  
 DT 30-JUL-1998 (first entry)  
 XX  
 DE cDNA encoding GAGE-5 tumour rejection antigen precursor.  
 XX  
 KW GAGE tumour rejection antigen precursor; TRAP; tumour; diagnosis;  
 KW melanoma; antigen; cytolytic T cell clone proliferation;  
 KW HLA-typing assay; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 75..429  
 FT /\*tag= a  
 FT /transl\_except= (pos:189..191, aa:Ala)  
 FT /transl\_except= (pos:192..194, aa:Thr)  
 PN WO9749417-A1.  
 XX  
 PD 31-DEC-1997.  
 XX  
 PF 23-JUN-1997; 97WO-US010850.  
 XX  
 PR 24-JUN-1996; 96US-00669161.  
 XX  
 FA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Debacker O, Van Den Eynde B, Boon-Falleur T;  
 XX  
 DR WPI; 1998-076905/07.  
 DR P-PSDB; AAW47602.  
 XX  
 PT Isolated nucleic acid encoding GAGE tumour rejection antigen precursor -  
 PT processed by HLA-Cw6 molecules into peptides, useful to diagnose  
 PT melanomas.  
 XX  
 PS Example 13; Fig 4; 60pp; English.  
 XX  
 CC The present sequence encodes a GAGE-5 tumour tumour rejection antigen  
 CC precursor (TRAP). The protein is expressed in a number of tumours. In  
 CC contrast the only normal tissue which expresses GAGE TRAP protein is  
 CC testis. Several GAGE TRAPs have been identified (see AAV18717-21). The  
 CC major difference between these proteins and GAGE-1 (AAV05540) is the  
 CC absence of a stretch of 143 bases located at position 379 to 521 of the  
 CC GAGE-1 TRAP sequence. The rest of the sequences show mismatches at  
 CC various position, with the exception of GAGE-3 whose 5' end is totally  
 CC different from the other GAGE cDNAs for the first 112 bases. This region  
 CC of GAGE-3 cDNA contains a long repeat and a hairpin structure. The  
 CC antigens can be used to diagnose melanomas, characterised by expression  
 CC of a TRAP or presentation of a tumour rejection antigen. Antigens shed  
 CC into blood or urine can be observed and then used to confirm a diagnosis



```

CC of melanoma using cytolytic T cell clone proliferation methodologies.
CC Other uses for the processed peptides, include HLA-typing assays for,
CC e.g. skin graft or organ transplants
XX
SQ Sequence 532 BP; 154 A; 110 C; 156 G; 112 T; 0 U; 0 Other;

  Query Match      92.3%; Score 496.8; DB 2; Length 532;
  Best Local Similarity 97.2%; Pred. No. 5.6e-134;
  Matches 517; Conservative 0; Mismatches 12; Indels 3; Gaps 1;

  QY 10 AGCTGTGAGGACGTCTGTGTGGTTCCTGCGGTCGGACTCTTTTCCTCTACTGAGATT 69
  Db 1 AGCTGTGAGGACGTCTGTGTGGTTCCTGCGGTCGGACTCTTTTCCTCTACTGAGATT 60
  QY 70 CATCTGTGTGAATATGAGTTCGCGAGGAAGATCGACC---TATCGGCTAGACCAAGAC 126
  Db CATCTGTGTGAATATGAGTTCGCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGC 120
  QY 127 GCTACGTAGAGCTCTCTGAAATGATTTGGGCTTATGCGGCCGAGCAGTTCAGTGTGAAG 186
  Db 121 GGTATGTACAGCTCTCTGAAGTGAATTTGGGCTTATGCGGCCGAGCAGTTCAGTGTGAAG 180
  QY 187 TGGAAACCAACAACACTGTAAGAAGGGGAACCAAGCAACTCAAGCTCAGGATCCTGCACTG 246
  Db 181 TGGAAACCAAGCTCTCTGAAGAAGGGGAACCAAGCAACTCAAGCTCAGGATCCTGCACTG 240
  QY 247 CTCAGAGGAGAGATGAGGAGCATCTGCAAGTCAAGGGCGAAGCCTGAAGTCTATA 306
  Db 241 CTCAGAGGAGAGATGAGGAGCATCTGCAAGTCAAGGGCGAAGCCTGAAGTCTATA 300
  QY 307 GCCAGGAACAGAGGTCAACCCACAGACTGGGTGTGAGTGTGAAGTGTCTGATGGCAGG 366
  Db 301 GCCAGGAACAGAGGTCAACCCACAGACTGGGTGTGAGTGTGAAGTGTCTGATGGCAGG 360
  QY 367 AGATGACCCGCCAAATCCAGAGGAGGTGAATAACCGCTGAAGAGGTGAAGAGCAATCAC 426
  Db 361 AGATGACCCGCCAAATCCAGAGGAGGTGAATAACCGCTGAAGAGGTGAAGAGCAATCAC 420
  QY 427 AGTGTAAAGAGACACCTTGAATATGATGCAAGGCTGCTCCTATGTTGAAATTTGTTCA 486
  Db 421 AGTGTAAAGAGACACCTTGAATATGATGCAAGGCTGCTCCTATGTTGAAATTTGTTCA 480
  QY 487 TTAATAATTCCTCCAAATAAAGCTTTACAGGCTTCTGCAAGAGAAAAA 538
  Db 481 TTAATAATTCCTCCAAATAAAGCTTTACAGGCTTCTGCAAGAGAAAAA 532

RESULT 9
AAV18717
ID AAV18717 standard; cDNA; 535 BP.
XX
AC AAV18717;

XX 30-JUL-1998 (first entry)
XX
XX cDNA encoding GAGE-2 tumour rejection antigen precursor.
XX
XX GAGE tumour rejection antigen precursor; TRAP; tumour; diagnosis;
XX melanoma; antigen; cytolytic T cell clone proliferation;
XX HLA-typing assay; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 81..431
XX FT /*tag= a
XX FT /transl_except= (pos:192..194, aa:Ala)
XX FT /transl_except= (pos:195..197, aa:Thr)
XX
XX WO9749417-A1.
XX
XX 31-DEC-1997.
XX

```

```

PF 23-JUN-1997; 97WO-US010850.
XX
PR 24-JUN-1996; 96US-00669161.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Debacker O, Van Den Eynde B, Boon-Palleur T;
XX
XX WPI; 1998-076905/07.
XX P-PSDB; AAW47599.
XX
XX Isolated nucleic acid encoding GAGE tumour rejection antigen precursor -
XX processed by HLA-Cw6 molecules into peptides, useful to diagnose
XX melanomas.
XX
XX Example 13; Fig 4; 60pp; English.
XX
XX The present sequence encodes a GAGE-2 tumour tumour rejection antigen
XX precursor (TRAP). The protein is expressed in a number of tumours. In
XX contrast the only normal tissue which expresses GAGE TRAP protein is
XX testis. Several GAGE TRAPs have been identified (see AAV18717-21). The
XX major difference between these proteins and GAGE-1 (AAV05540) is the
XX absence of a stretch of 143 bases located at position 379 to 521 of the
XX GAGE-1 TRAP sequence. The rest of the sequences show mismatches at
XX various position, with the exception of GAGE-3 whose 5' end is totally
XX different from the other GAGE cDNAs for the first 112 bases. This region
XX of GAGE-3 cDNA contains a long repeat and a hairpin structure. The
XX antigens can be used to diagnose melanomas, characterised by expression
XX of a TRAP or presentation of a tumour rejection antigen. Antigens shed
XX into blood or urine can be observed and then used to confirm a diagnosis
XX of melanoma using cytolytic T cell clone proliferation methodologies.
XX Other uses for the processed peptides, include HLA-typing assays for,
XX e.g. skin graft or organ transplants
XX
SQ Sequence 535 BP; 158 A; 112 C; 156 G; 109 T; 0 U; 0 Other;

  Query Match      91.6%; Score 493; DB 2; Length 535;
  Best Local Similarity 97.2%; Pred. No. 7.2e-133;
  Matches 524; Conservative 0; Mismatches 10; Indels 5; Gaps 2;

  QY 1 AGCCAGGAGGAGTGTGAGGACGTGTGTGGTTCCTGCGGTCGGACTCTTTTTCCTC- 59
  Db 1 AGCCAGGAGGAGTGTGAGGACGTGTGTGGTTCCTGCGGTCGGACTCTTTTTCCTC- 56
  QY 60 TACTGAGATTCACTGTGTGAAATATGAGTTGGCGAGGAAGATCACTATCGGCTAGA 119
  Db 57 TACTGAGATTCACTGTGTGAAATATGAGTTGGCGAGGAAGATCACTATCGGCTAGA 116
  QY 120 CCAAGACGCTAGTAGAGCTCTCGAATATGATTTGGGCTATCGGCGGAGAGTTCAGT 179
  Db 117 CCAAGACGCTAGTAGAGCTCTCGAATATGATTTGGGCTATCGGCGGAGAGTTCAGT 176
  QY 180 GATGAAGTGGAAACCAAGCAACCTCGAAGAGGGGAACCAAGCAACTCAAGCTCAGGATCCT 239
  Db 177 GATGAAGTGGAAACCAAGCAACCTCGAAGAGGGGAACCAAGCAACTCAAGCTCAGGATCCT 236
  QY 240 GCAGTGTCTCAGGAGGAGAGGATGAGGAGCAATCTGAGGTCAAGGGCCGAGGCTGAA 299
  Db 237 GCAGTGTCTCAGGAGGAGAGGATGAGGAGCAATCTGAGGTCAAGGGCCGAGGCTGAA 296
  QY 300 GCTCATAGCCAGGACAGGATCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCAT 359
  Db 297 GCTGAGAGCCAGGAAACAGGGGTCAACCACAGACTGGGTGTGAGTGTGAAGATGGTCTCAT 356
  QY 360 GGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAACCGCCTGAAGAGTGAAGAG 419
  Db 357 GGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAACCGCCTGAAGAGTGAAGAG 416
  QY 420 CAATCAGAGTGTAAAGAGAGACAGCTTGAATATGATGAGGCTGTCTCTATGTTGGAAT 479
  Db 417 CAATCAGAGTGTAAAGAGAGACAGCTTGAATATGATGAGGCTGTCTCTATGTTGGAAT 476
  QY 480 TTGTTTATTAATAATTCCTCCCAATAAAGCTTTTACAGCTTCTGCAAGAGAAAAA 538

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Db 477 TTGTCATTAAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA 535
|||||
RESULT 10
ADA15802
ID ADA15802 standard; cDNA; 526 BP.
XX
XX
AC ADA15802;
XX
XX 06-NOV-2003 (first entry)
XX
XX Human GAGE-7B cDNA.
XX
XX Human; GAGE-7B; gene; ss; cytolytic T lymphocyte; CTL;
XX human leukocyte antigen; HLA; tumour rejection antigen precursor;
XX major histocompatibility complex; MHC; cytolytic T cell proliferation;
XX chromosome Xp11.2-p11.4.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 55..408
XX /*tag= a
XX /product= "Human GAGE-7B"
XX /transl_except= (pos:115..162, aa: GPMRPEOGSDVPSMI)
XX /transl_except= (pos:265..306, aa: HPQTGKEAHSEQ)
XX
XX US6509172-B1.
XX
XX 21-JAN-2003. 98US-00163748.
XX
XX 30-SEP-1998; 98US-00163748.
XX
XX 30-SEP-1998; 98US-00163748.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX De Backer O, Van Den Eynde B, Boon-Falleur T;
XX
XX WPI; 2003-401119/38.
XX
XX P-PSDB; ADA15777.
XX
XX New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tumor
XX rejection antigen precursors, which complex to major histocompatibility
XX complex molecules to facilitate the proliferation of cytolytic T cells.
XX
XX Claim 1; Col 9-10; 15pp; English.
XX
XX The invention relates to isolated GAGE-7B and GAGE-8 polypeptides and the
XX nucleic acid molecules encoding them. The invention also relates to an
XX expression vector comprising an isolated nucleic acid molecule of the
XX invention operably linked to a promoter, a recombinant cell comprising
XX the isolated nucleic acid molecule or the expression vector and an
XX expression kit useful in generating cytolytic T lymphocytes (CTLs) or
XX determining if CTLs are present in a sample comprising the isolated
XX nucleic acid molecule and the isolated nucleic acid that encodes a human
XX leukocyte antigen (HLA) molecule. The GAGE-7B and GAGE-8 nucleic acid
XX molecules encode tumour rejection antigen precursors, which complex to
XX major histocompatibility complex (MHC) molecules to facilitate the
XX proliferation of cytolytic T cells. This sequence represents cDNA
XX encoding the human GAGE-7B polypeptide of the invention. The gene resides
XX on chromosome Xp11.2-p11.4.
XX
XX Sequence 526 BP; 168 A; 109 C; 143 G; 106 T; 0 U; 0 Other;
XX
XX Query Match 90.7%; Score 488; DB 7; Length 526;
XX Best Local Similarity 98.4%; Pred. No. 2e-131;
XX Matches 504; Conservative 0; Mismatches 5; Indels 3; Gaps 1;
XX
XX 30 TGGTCTCGCGCTCGGACTCTTTTCTCTACTGAGATTTCATCTGTGTAATATGAGT 89
|||||
Db 1 TGGTCCGCGCTCGGACTCTTTTCTCTACTGAGATTTCATCTGTGTAATATGAGT 60
```

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QY 90 TGGCGAGGAAGATCGACC---TATCGCCTAGACCAGCGCTAGAGCCTCTCTGAA 146
Db 61 TGGCGAGGAAGATCGACCTATTATTGGCCCTAGACCAGGCGCTATGTACAGCCTCTGAA 120
QY 147 ATGATTGGGCTTATGGGCCCGAGCAGTTCAGTGAATGGAACCAACACCTGAA 206
Db 121 ATGATTGGGCTTATGGGCCCGAGCAGTTCAGTGAATGGAACCAACACCTGAA 180
QY 207 GAAGGGGAACCAAGCACTCAACGTCAAGATCCTGAGCTGCTCAGGAGGAGAGGATGAG 266
Db 181 GAAGGGGAACCAAGCACTCAACGTCAAGATCCTGAGCTGCTCAGGAGGAGAGGATGAG 240
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QY 387 GAGGAGGTGAAAACGGCTGAAGAGGTGAAAAGCAATCACAGTCTTAAAGAGACACAGT 446
Db 361 GAGGAGGTGAAAACGGCTGAAGAGGTGAAAAGCAATCACAGTCTTAAAGAGAGGACAGT 420
QY 447 TGAATGATGACAGGCTGCTCTCTATGTTGGAAATTTGTTCAATTAATAATCTCCCAATAAAG 506
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## RESULT 11

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ID AAC02129 standard; cDNA; 430 BP.
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XX AAC02129;
XX
XX 06-OCT-2000 (first entry)
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XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.
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XX Homo sapiens.
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XX EPI033401-A2.
XX
XX 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-00200610.
XX
XX 26-FEB-1999; 99US-0122487P.
XX
XX (BEST ) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX WPI; 2000-500381/45.
XX
XX P-PSDB; AAG02123.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
XX Claim 1; SEQ ID NO 2127; 71pp + Sequence Listing; English.
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CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. An ORF has been identified within the
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
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Db	137	CAAGACGCTACCTAGAGCCTCTGAAATGATTGGGCTATGGGCGGAGCAGTTCAGTG	196
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QY	241	CAG 243	
Db	257	CAG 259	

RESULT 15  
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ID ABZ19533 standard; cDNA; 225 BP.  
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DT 23-JAN-2003 (first entry)  
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DE Group III cDNA cancer related clone SEQ ID NO:1959.  
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DE Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;  
KW immune response; virology; immunology; microbiology; molecular biology;  
KW recombinant DNA technology; gene; ss.  
XX  
OS Homo sapiens.  
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PN WO2002/78516-A2.  
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PD 10-OCT-2002.  
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PF 28-MAR-2002; 2002WO-US010421.  
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PR 30-MAR-2001; 2001US-0280255P.  
PR 28-AUG-2001; 2001US-0315563P.  
PR 09-JAN-2002; 2002US-0347313P.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Wang T, Wang S, Bangur CS, Gaiger A;  
XX  
DR WPI; 2003-058387/05.

New immunogenic polynucleotides or polypeptides useful for diagnosing, preventing and treating cancer expressing CT or CP mRNA antigens, and in virology, immunology, microbiology, molecular biology and recombinant DNA techniques.  
Claim 1; SEQ ID NO 1959; 207pp; English.

ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and ABP54446 to ABP54472 represent protein (II) sequences, from the present invention. (I) and (II) have cytostatic activity and can be used in gene therapy and vaccines. (i), (ii), antibodies and compositions from the present invention are useful for diagnosing, preventing and treating cancer, which expresses CT or CP mRNA antigens. They are useful for stimulating immune response. They can also be useful in virology, immunology, microbiology, molecular biology and recombinant DNA techniques. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Query Match 41.8%; Score 225; DB 7; Length 225;  
Best Local Similarity 100.0%; Pred. No. 3.7e-55;  
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	19	GCAGTGCCTGTGGTTCCTGCGGAGATCGACTATCGGCCTAGACCAAGACGCTACGTAGAGC	138
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Job time : 378 secs

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QY	199	CACCTGAAGAGGGGAACCAAGCAACTCAACGTCAGGATCCTGCAG	243
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues  
Total number of hits satisfying chosen parameters: 3980872

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
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- 40: em.hgo.mus.\*
- 41: em.hgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
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SUMMARIES

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3	538	100.0	538	6	I55851	Sequence 14	
4	538	100.0	538	6	BD132467	Isolated,	
5	530	98.5	530	9	HSU19143	Human GAGE-	
6	525.4	97.7	528	6	AR275665	Sequence	
7	525.4	97.7	528	9	AF055473	Homo sapi	
8	504.8	93.8	532	6	AR028491	Sequence	
9	504.8	93.8	532	6	BD231800	Isolated	
10	504.8	93.8	532	6	I55854	Sequence 17	
11	504.8	93.8	532	6	BD132470	Isolated,	
12	501.4	93.2	528	6	AX334151	Sequence	
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19	357.8	66.5	430	6	AX886264	Sequence	
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C	22	299.2	55.6	365	6	AX284692	Sequence
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27	149	27.7	441	12	BT007722	Synthetic	
28	141	26.2	524	6	AR416095	Sequence	
29	141	26.2	524	6	BD111648	EST and e	
30	132.8	24.7	494	6	AR416094	Sequence	
31	132.8	24.7	494	6	BD111647	EST and e	
32	130.4	24.2	475	6	AX226497	Sequence	
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37	108	20.1	399	6	AR272357	Sequence	
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LOCUS	Sequence 14 from patent US 5858689.					
DEFINITION	Sequence 14 from patent US 5858689.					
ACCESSION	AR028488					
VERSION	AR028488.1	GI:5940461				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 538)					
AUTHORS	van der Bruggen, P., van den Bynde, B., DeBacker, O. and Boon-Falleur, T.					
TITLE	Isolated peptides derived from the gage tumor rejection antigen precursor and uses thereof					







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Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241  CAGCTGCTCAGGAGGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGGAAGCCTGAAG 300
Db 241  CAGCTGCTCAGGAGGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGGAAGCCTGAAG 300

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QY 481  TGTTCATTAAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAA 530
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RESULT 6
AR275665 LOCUS
DEFINITION Homo sapiens GAGE-8 mRNA, complete cds.
ACCESSION AF055473
VERSION AF055473.1 GI:3511022
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 528)
AUTHORS De Backer, O., Van den Eynde, B. and Boon-Palleur, T.
TITLE Isolated, truncated nucleic acid which are members of the gage, and
JOURNAL uses thereof
PATENT: US 6509172-A 1 21-JAN-2003;
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QY 132  GTGAGAGCTCTGAAATGATTGGCCCTATCGGCCCGGAGGATTCAGTGATGAAGTGAA 191
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QY 192  CCAGCAACCTGAAGAGGGGAAACAGCAACTCAACGTCAAGATCCTGCAGCTGCTCAG 251
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QY 252  GAGGAGAGGATGAGGAGGATCTGCAGGTCAAGGGCCGAGCCTGAAGCTCATAGCCAG 311
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QY 312  GAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTGATGGCAGAGATG 371
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QY 372  GACCCGCCAATCCAGAGGAGGTGAAACCGCTCAAGAAAGGTGAAAAGCAATCAAGTGT 431
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DEFINITION Homo sapiens GAGE-8 mRNA, complete cds.
ACCESSION AF055473
VERSION AF055473.1 GI:3511022
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 528)
AUTHORS De Backer, O., Boretta, M., Vantomme, V., De Smet, C.,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 528)
AUTHORS De Backer, O., Arden, K.C., Boretta, M., Vantomme, V., De Smet, C.,
Czekay, S., Viars, C.S., De Plaen, E., Brasseur, F., Chomez, P., Van den
Eynde, B., Boon, I. and van der Bruggen, P.
TITLE Characterization of the GAGE genes that are expressed in various
JOURNAL human cancers and in normal testis
MEDLINE Cancer Res. 59 (13), 3157-3165 (1999)
PUBMED 99323388
REFERENCE 2 (bases 1 to 528)
AUTHORS De Backer, O.R.Y.
TITLE Direct Submission
JOURNAL Submitted (24-MAR-1998) Ludwig Institute for Cancer Research,
Brussels Branch, 74 av. Hippocrate, Brussels B-1200, Belgium
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LOCUS BDI32470 532 bp DNA linear PAT 18-SEP-2002
DEFINITION Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof.
ACCESSION BDI32470.1 GI:23227415
VERSION BDI32470.1
KEYWORDS JP 2002507112-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 532)
AUTHORS DeBacker,O., Eynde,B.V.D. and Falleur,T.B.
TITLE Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof
JOURNAL Patent: JP 2002507112-A 10 05-MAR-2002;
COMMENT LUDWIG INSTITUTE FOR CANCER RESEARCH
PN JP 2002507112-A/10
PD 05-MAR-2002
PF 23-JUN-1997 JP 1998503430
PR 24-JUN-1996 US 08/669161
PI OLIVIER DEBACKER,BENOIT VAN DEN EYNDE,THIERRY BOON FALLEUR PC
AG1K38/00,AG1K45/05,C07K7/00,C07K14/82,C12N15/00 CC
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DEFINITION Sequence 17 from patent US 5648226.
ACCESSION I55854
VERSION I55854.1
KEYWORDS GI:2476648
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 532)
AUTHORS Van den Eynde,B., DeBacker,O. and Boon-Falleur,T.
TITLE Isolated peptides derived from tumor rejection antigens, and their use
JOURNAL Patent: US 5648226-A 17 15-JUL-1997;
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QY 487 TTAATAATCTCCAAATAAGCTTTACAGCCTTCTGCAAGAAAAAATAAAAAA 538
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AUTHORS
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QY 2 CGCCAGGAGCTGTGAGGAGTCTGTGTGTTCTCGCGTCCGAGTCTTTTCTCTCA 61
Db 1 CGCCAGGAGCTGTGAGGAGTCTGTGTGTTCTCGCGTCCGAGTCTTTTCTCTCA 60

us-09-782-745-14.closed.rge
Page 7
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## EVKTPBEQKQSQC"

## ORIGIN

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Best Local Similarity 98.3%; Pred. No. 3.4e-114;  
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QY 119 ACCAGAGCTACGTAGAGCTCTCTGAATGATTGGGCTATGGGCCGAGAGCTTACAG 178  
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HSU19147  
LOCUS Human GAGE-6 protein mRNA, complete cds.  
DEFINITION U19147  
ACCESSION U19147.1 GI:914908  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 527)  
AUTHORS Van den Eynde, B., Peeters, O., De Backer, O., Gaugler, B., Lucas, S., and Boon, T.  
TITLE A new family of genes coding for an antigen recognized by autologous cytolytic T lymphocytes on a human melanoma  
J. Exp. Med. 182 (3), 689-698 (1995)  
PUBMED 95378788  
REFERENCE 2 (bases 1 to 527)  
AUTHORS Van den Eynde, B.J.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium  
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AP058988  
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DEFINITION AP058988  
ACCESSION AP058988.1 GI:3300089  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 524)  
AUTHORS Chen, M.E., Lin, S.-H., Chung, L.W.K. and Sikes, R.A.  
TITLE Isolation and characterization of PAGE-1 and GAGE-7: new genes expressed in the LNCap prostate cancer progression model that share homology with melanoma associated antigens  
J. Biol. Chem. (1998) In press  
REFERENCE 2 (bases 1 to 524)



AUTHORS Chen, M.E., Lin, S.-H., Chung, L.W.K. and Sikes, R.A.  
TITLE Direct Submission  
JOURNAL Submitted (07-APR-1998) Urology, University of Virginia, Box 422,  
Charlottesville, VA 22908, USA  
FEATURES Location/Qualifiers  
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## ORIGIN

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Best Local Similarity 97.9%; Pred. No. 3e-113;  
Matches 513; Conservative 2; Mismatches 6; Indels 3; Gaps 1;  
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QY 65 AGATTTCATCTGTGAAATATAGTTGCGGAGAGATCGACC--TATCGGCTAGACC 121  
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QY 122 AAGACCTAGTGTAGGCTCTCTGAAATGATGTGGGCTATGCGGCTCGGAGAGTTCAGTGA 181  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-782-745-15  
Perfect score: 560  
Sequence: 1 CTCATATTCACACAGATCA.....CTGCAGAGAAAAA 560

Scoring table: IDENTITY\_NUC  
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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 4080270

Minimum DB seq length: 0  
Maximum DB seq length: 560

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
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- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	560	100.0	560	6	AR028489	AR028489 Sequence
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4	560	100.0	560	6	BD132468	BD132468 Isolated,
5	552	98.6	552	9	HSU19144	U19144 Human GAGE-
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8	446.4	79.7	532	6	I55854	I55854 Sequence 17
9	446.4	79.7	532	6	BD132470	BD132470 Isolated,
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14	443.2	79.1	540	6	I55853	I55853 Sequence 16
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37	169	30.2	548	9	BC062680	BC062680 Homo sapi
38	166.6	29.8	550	6	AX921769	AX921769 Sequence
39	164	29.3	493	9	HSR318881	HSR318881 Sequence
40	157.2	28.1	494	6	AX921771	AX921771 Sequence
41	150.6	26.9	441	12	BT007722	BT007722 Synthetic
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ALIGNMENTS

RESULT 1	AR028489	AR028489	560 bp	DNA	linear	PAT 29-SEP-1999
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DEFINITION	Sequence 15 from patent US 5856689.					
ACCESSION	AR028489					
VERSION	AR028489.1	GI:5940462				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 560)					
AUTHORS	van der Bruggen,P., van den Eynde,B., DeBacker,O. and Boon-Falleur,T.					
TITLE	Isolated peptides derived from the gage tumor rejection antigen precursor and uses thereof					

JOURNAL Patent: US 5858689-A 15 12-JAN-1999;  
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ORIGIN

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LOCUS Isolated polypeptides binding with HLA-A29 molecule, nucleic acids  
DEFINITION as molecules encoding the same, and utilization thereof.  
ACCESSION BD231798  
VERSION BD231798.1 GI:33041568  
KEYWORDS JP 2002509859-A/8.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 560)  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Bruggen,P.V.D., Eynde,B.V.D., Debacker,O. and Falleur,T.B.  
AUTHORS Isolated polypeptides binding with HLA-A29 molecule, nucleic acids  
TITLE as molecules encoding the same, and utilization thereof  
JOURNAL Patent: JP 2002509859-A 8 02-APR-2002;  
LUDWIG INSTITUTE FOR CANCER RESEARCH  
COMMENT OS Homo sapiens (human)  
PN JP 2002509859-A/8  
PD 02-APR-2002

PF 12-JAN-1999 JP 2000528586  
PR 23-JAN-1998 US 09/012818  
PI PIERRE VAN DER BRUGGEN,BENOIT VAN DEN EYNDE,OLIVIER DEBACKER,  
THIERRY BOON FALLEUR  
PC C07K4/12,C12N15/09,C12P21/00,C12Q1/02,C12N15/00 CC  
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CC Topology: Linear;  
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FH Key Location/Qualifiers  
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ORIGIN

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Db 301 GGTCAAGGGCCGAGCGCTGATGAGTGAACACAGCAACCTGAAGAGGGGAAACCA 360  
Qy 361 GAGTGTGAAGATGTCCTGATGGGAGGAGATGGAACCGCAATCCAGAGGAGGTGAAA 420  
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Qy 421 ACGCTGAAGAGGTGAAGCAATCAGTGTAAAGAGGAGGAGGAGGAGCATCTGCA 480  
Db 421 ACGCTGAAGAGGTGAAGCAATCAGTGTAAAGAGGAGGAGGAGGAGCATCTGCA 480  
Qy 481 GGCTGCTCCTATGTTGGAAATTTGTCATTAATAATTCCTCCCAATAAAGCTTTACAGCCTT 540  
Db 481 GGCTGCTCCTATGTTGGAAATTTGTCATTAATAATTCCTCCCAATAAAGCTTTACAGCCTT 540  
Qy 541 CTGCAAGAGAAAAA 560  
Db 541 CTGCAAGAGAAAAA 560

RESULT 3

I55852  
LOCUS I55852  
DEFINITION Sequence 15 from patent US 5648226.  
ACCESSION I55852  
VERSION I55852.1  
KEYWORDS GI:2476646  
SOURCE Unknown.  
ORGANISM Unkown.  
Unclassified.

REFERENCE 1 (bases 1 to 560)  
AUTHORS Van den Eynde,B., DeBacker,O. and Boon-Falleur,T.  
TITLE Isolated peptides derived from tumor rejection antigens, and their use  
JOURNAL Patent: US 5648226-A 15 15-JUL-1997;  
FEATURES Location/Qualifiers  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 7.3e-137;  
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 421 ACGCCTGAAGAGGTGAAGAGCAATCACAGTGTATAAAGAGGCAGCTTGAATGATGCA 480  
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QY 541 CTGCAAGAAAAA 560  
Db 541 CTGCAAGAAAAA 560

RESULT 4  
BD132468  
LOCUS BD132468  
DEFINITION Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, and uses thereof.  
ACCESSION BD132468  
VERSION BD132468.1 GI:23227413  
KEYWORDS JP 2002507112-A/8.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 560)  
AUTHORS Debacker,O., Eynde,B.V.D. and Falleur,T.B.  
TITLE Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof  
JOURNAL Patent: JP 2002507112-A 8 05-MAR-2002;  
LUDWIG INSTITUTE FOR CANCER RESEARCH

COMMENT PN JP 2002507112-A/8  
PD 05-MAR-2002  
PF 23-JUN-1997 JP 1998503430  
PR 24-JUN-1996 US 08/669161  
PI OLIVIER DEBACKER,BENOIT VAN DEN EYNDE,THIERRY BOON FALLEUR PC  
A61K38/00,A61K45/05,C07K7/00,C07K14/82,C12N15/00 CC  
Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers.  
FEATURES Location/Qualifiers  
source 1..560  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN  
Query Match 100.0%; Score 560; DB 6; Length 560;  
Best Local Similarity 100.0%; Pred. No. 7.3e-137;  
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCATATTTCACACAGATGAGTTGGCGAGAGATCGACCTATTATTGCTTAGGCCAAT 60  
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QY 361 GAGTGTGAAGATGGTCTGATGGCGAGAGATGGACCCGCCAAATCCAGAGAGGTGAAA 420  
Db 361 GAGTGTGAAGATGGTCTGATGGCGAGAGATGGACCCGCCAAATCCAGAGAGGTGAAA 420  
QY 421 ACGCCTGAAGAGGTGAAGAGCAATCACAGTGTATAAAGAGGCAGCTTGAATGATGCA 480  
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QY 481 GGCTGCTCCTATGTTGGAAATTTGTTCAATTAATAATTTCTCCCAATAAGCTTTACAGCCTT 540  
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QY 541 CTGCAAGAAAAA 560  
Db 541 CTGCAAGAAAAA 560

RESULT 5  
HSU19144  
LOCUS HSU19144  
DEFINITION Human GAGE-3 protein mRNA, complete cds.  
ACCESSION U19144  
VERSION U19144.1 GI:914902  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 552)

AUTHORS Van den Eynde, B., Peeters, O., De Backer, O., Gaugler, B., Lucas, S. and Boon, T.  
TITLE A new family of genes coding for an antigen recognized by autologous cytolytic T lymphocytes on a human melanoma  
J. Exp. Med. 182 (3), 689-698 (1995)  
MEDLINE 95378788  
PUBMED 7544395  
REFERENCE 2 (bases 1 to 552)  
AUTHORS Van den Eynde, B.J.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-1994) Benoit J Van den Eynde, Ludwig Institute For Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium  
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/sex="female"  
/cell\_line="M22-MEL.43"  
/tissue\_type="melanoma"  
/dev\_stage="adult"  
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/db\_xref="GI:914903"  
/translation="MNLSRGKSTVYWPBRBYVOPPEVIGPMRPEQFSDEVPATPEE  
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ORIGIN  
Query Match 98.6%; Score 552; DB 9; Length 552;  
Best Local Similarity 100.0%; Pred. No. 9.4e-135; Indels 0; Gaps 0;  
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DB 361 GAGTGTGAAGTGTCTCTGATGGGAGGAGATGAGTGAACCGCCCAATCCAGAGAGGTGAAA 420  
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QY 481 GGCTGCTCTTATGTTGGAATTTGTTTCAATTAATTTCTCCCAATAAGCTTTTACAGCCTT 540  
DB 481 GGCTGCTCTTATGTTGGAATTTGTTTCAATTAATTTCTCCCAATAAGCTTTTACAGCCTT 540  
QY 541 CTGCAAGAGAAA 552  
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Db 541 CTGCAAGAGAAA 552  
RESULT 6  
LOCUS AR028491  
DEFINITION Sequence 17 from patent US 5858689.  
ACCESSION AR028491  
VERSION AR028491.1 GI:5940464  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 532)  
AUTHORS van der Bruggen, P., van den Eynde, B., DeBacker, O. and Boon-Falleur, T.  
TITLE Isolated peptides derived from the gage tumor rejection antigen precursor and uses thereof  
JOURNAL Patent: US 5858689-A 17 12-JAN-1999;  
FEATURES  
source  
1..532  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 79.7%; Score 446.4; DB 6; Length 532;  
Best Local Similarity 99.8%; Pred. No. 7e-107; Indels 0; Gaps 0;  
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 113 GAGAAATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTCTGAAGTGA 172  
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QY 173 TTGGCCCTATGCGGCCGACGAGTTTCAGTATGAAGTGAACCAACGACCTGAAGAAG 232  
DB 145 TTGGCCCTATGCGGCCGACGAGTTTCAGTATGAAGTGAACCAACGACCTGAAGAAG 204  
QY 233 GGAACACAGCAACTCAACGTCAGGATCCTCAGCTCAGTCTCAGGAGGAGAGATGAGGAG 292  
DB 205 GGAACACAGCAACTCAACGTCAGGATCCTCAGCTCAGTCTCAGGAGGAGAGATGAGGAG 264  
QY 293 CATCTCAGCTCAAGGCCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCAACCCACAGA 352  
DB 265 CATCTCAGCTCAAGGCCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCAACCCACAGA 324  
QY 353 CTGGGTGTGAGTGTGAAGATGGTCTCAGTGGGAGGAGATGGACCCCAATCCAGAGG 412  
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QY 413 AGGTGAAAACGCTCTGAAGAGAGTGAAGCAATCAACAGTGTAAAGAGAGGACGTTGAA 472  
DB 385 AGGTGAAAACGCTCTGAAGAGAGTGAAGCAATCAACAGTGTAAAGAGAGGACGTTGAA 444  
QY 473 ATGATCAGGCTGCTCTCTATGTTGGAAATTTGTTTCAATTAATTTCTCCCAATAAGCTTT 532  
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QY 533 ACAGCTTCTGCAAG 560  
DB 505 ACAGCTTCTGCAAG 532  
RESULT 7  
LOCUS BD231800  
DEFINITION Isolated polypeptides binding with HLA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof.  
ACCESSION BD231800  
VERSION BD231800.1 GI:33041570  
KEYWORDS JP 2002509859-A/10.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 532)  
AUTHORS Bruggen,F.V.D., Eynde,B.V.D., DeBacker,O. and Falleur,T.B.  
TITLE Isolated polypeptides binding with HUA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof  
JOURNAL Patent: JP 2002509859-A 10 02-APR-2002;  
COMMENT LUDWIG INSTITUTE FOR CANCER RESEARCH  
OS Homo sapiens (human)  
PN JP 2002509859-A/10  
PD 02-APR-2002  
PF 12-JAN-1999 JP 2000528586  
PI 23-JAN-1998 US 09/012818  
PI PIERRE VAN DER BRUGEN,BENOIT VAN DEN EYNDE,OLIVIER DEBACKER,  
PI THIERRY BOON FALLEUR  
PC C07K4/12,C12N15/09,C12P21/00,C12Q1/02,C12N15/00 CC  
Strandedness: Single;  
CC Topology: Linear;  
CC STRANDEDNESS:single,TOPOLOGY:linear  
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FT source 1..532 /organism='Homo sapiens (human)'.  
FEATURES  
source Location/Qualifiers  
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/db\_xref="taxon:9606"  
ORIGIN  
Query Match 79.7%; Score 446.4; DB 6; Length 532;  
Best Local Similarity 99.8%; Pred. No. 7e-107;  
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 113 GAGGAAATCGACCTATTATTGGCTAGACCAAGCGCTATGACAGCCTCCTGAAGTGA 172  
DB 85 GAGGAAGATCGACCTATTATTGGCTAGACCAAGCGCTATGACAGCCTCCTGAAGTGA 144  
QY 173 TTGGGCTATGCGGCCGCGAGCTTCAGTGATGAAGTGAAGTGAACCAACCTGAAGAAG 232  
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QY 233 GGAACCAAGCACTCAACGTCAGGATCTGACAGTCTCAGGAGGAGGATGAGGGAG 292  
DB 205 GGAACCAAGCACTCAACGTCAGGATCTGACAGTCTCAGGAGGAGGATGAGGGAG 264  
QY 293 CATCTGCAGGTCAAGGGCCGAGCCTGAAGTGTAGTGAAGTGAAGTGAAGTGAAGTGA 352  
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DB 325 CTGGGTGTGAGTGTGAAGATGTCCTGTATGGCAGGAGATGACCCGCCAATCCAGAGG 384  
QY 413 AGGTGAAAACCGCTCAAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGTGA 472  
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QY 473 ATGATGCAGGCTGCTCTATGTTGGAATTTCTTCAATAAAATTCCTCCCAATAAAGCTTT 532  
DB 445 ATGATGCAGGCTGCTCTATGTTGGAATTTCTTCAATAAAATTCCTCCCAATAAAGCTTT 504  
QY 533 ACAGCCTTCTGCAAGAAAAA 560  
DB 505 ACAGCCTTCTGCAAGAAAAA 532  
RESULT 9  
BD132470 532 bp DNA linear PAT 18-SBP-2002  
LOCUS Isolated, nucleic acid molecules which code for GAGE tumor  
DEFINITION rejection antigen, the tumor rejection antigen, and uses thereof.  
ACCESSION BD132470  
VERSION BD132470.1 GI:23227415  
KEYWORDS JP 2002507112-A/10.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 532)  
AUTHORS Debacker,O., Eynde,B.V.D. and Falleur,T.B.  
TITLE Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof  
JOURNAL Patent: JP 2002507112-A 10 05-MAR-2002;  
COMMENT LUDWIG INSTITUTE FOR CANCER RESEARCH  
PN JP 2002507112-A/10  
PD 05-MAR-2002  
PF 23-JUN-1997 JP 1998503430  
PI 24-JUN-1996 US 08/669161  
PI OLIVIER DEBACKER,BENOIT VAN DEN EYNDE,THIERRY BOON FALLEUR PC  
A61K38/00,A61K45/05,C07K7/00,C07K14/82,C12N15/00 CC

ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 532)  
AUTHORS Van den Eynde,B., DeBacker,O. and Boon-Falleur,T.  
TITLE Isolated peptides derived from tumor rejection antigens, and their use  
JOURNAL Patent: US 5648226-A 17 15-JUL-1997;  
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source Location/Qualifiers  
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ORIGIN  
Query Match 79.7%; Score 446.4; DB 6; Length 532;  
Best Local Similarity 99.8%; Pred. No. 7e-107;  
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 113 GAGGAAATCGACCTATTATTGGCTAGACCAAGCGCTATGACAGCCTCCTGAAGTGA 172  
DB 85 GAGGAAGATCGACCTATTATTGGCTAGACCAAGCGCTATGACAGCCTCCTGAAGTGA 144  
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QY 233 GGAACCAAGCACTCAACGTCAGGATCTGACAGTCTCAGGAGGAGGATGAGGGAG 292  
DB 205 GGAACCAAGCACTCAACGTCAGGATCTGACAGTCTCAGGAGGAGGATGAGGGAG 264  
QY 293 CATCTGCAGGTCAAGGGCCGAGCCTGAAGTGTAGTGAAGTGAAGTGAAGTGAAGTGA 352  
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DB 505 ACAGCCTTCTGCAAGAAAAA 532  
RESULT 9  
BD132470 532 bp DNA linear PAT 18-SBP-2002  
LOCUS Isolated, nucleic acid molecules which code for GAGE tumor  
DEFINITION rejection antigen, the tumor rejection antigen, and uses thereof.  
ACCESSION BD132470  
VERSION BD132470.1 GI:23227415  
KEYWORDS JP 2002507112-A/10.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 532)  
AUTHORS Debacker,O., Eynde,B.V.D. and Falleur,T.B.  
TITLE Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof  
JOURNAL Patent: JP 2002507112-A 10 05-MAR-2002;  
COMMENT LUDWIG INSTITUTE FOR CANCER RESEARCH  
PN JP 2002507112-A/10  
PD 05-MAR-2002  
PF 23-JUN-1997 JP 1998503430  
PI 24-JUN-1996 US 08/669161  
PI OLIVIER DEBACKER,BENOIT VAN DEN EYNDE,THIERRY BOON FALLEUR PC  
A61K38/00,A61K45/05,C07K7/00,C07K14/82,C12N15/00 CC

Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers.  
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1. .532  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

## ORIGIN

Query Match 79.7%; Score 446.4; DB 6; Length 532;  
Best Local Similarity 99.8%; Pred. No. 7e-107;  
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 113 GAGGAAATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCCTCAAGTGA 172  
DB 85 GAGGAAATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCCTCAAGTGA 144  
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DB 145 TTGGGCTTATCGGCGCCGAGCAGTTTCAGTGTAGTGAAGTGAACACGACCTGAAGAAG 204  
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QY 473 ATGATGACGCTGTCTCTATGTTGGAATTTGTTTCAATAAATTTCTCCCAATAAGCTTT 532  
DB 445 ATGATGACGCTGTCTCTATGTTGGAATTTGTTTCAATAAATTTCTCCCAATAAGCTTT 504  
QY 533 ACAGCTTCTGCAAG 560  
DB 505 ACAGCTTCTGCAAG 532

RESULT 10  
AR275666  
LOCUS AR275666 526 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 2 from patent US 6509172.  
ACCESSION AR275666  
VERSION AR275666.1 GI:29709168  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 526)  
AUTHORS De Backer, O., Van den Eynde, B. and Boon-Falleur, T.  
TITLE Isolated, truncated nucleic acid which are members of the gage, and uses thereof  
JOURNAL Patent: US 6509172-A 2 21-JAN-2003;  
FEATURES  
source  
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## ORIGIN

Query Match 79.1%; Score 443.2; DB 6; Length 526;  
Best Local Similarity 99.3%; Pred. No. 4.9e-106;  
Matches 445; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 113 GAGGAAATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCCTCAAGTGA 172

DB 65 GAGGAAATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCCTCAAGTGA 124  
QY 173 TTGGGCTTATCGGCGCCGAGCAGTTTCAGTGTAGTGAAGTGAACACGACCTGAAGAAG 232  
DB 125 TTGGGCTTATCGGCGCCGAGCAGTTTCAGTGTAGTGAAGTGAACACGACCTGAAGAAG 184  
QY 233 GGGACACGACCACTCAAGCTCAGATCTGAGTGTGAGTGAAGTGAACACGACCTGAAGAAG 292  
DB 185 GGGACACGACCACTCAAGCTCAGATCTGAGTGTGAGTGAAGTGAACACGACCTGAAGAAG 244  
QY 293 CATCTGACGCTCAAGGCGGAGGCTGAGTGTGAGTGAAGTGAACACGACCTGAAGAAG 352  
DB 245 CATCTGACGCTCAAGGCGGAGGCTGAGTGTGAGTGAAGTGAACACGACCTGAAGAAG 304  
QY 353 CTGGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 412  
DB 305 CTGGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 364  
QY 413 AGTGTGAACCCCTGAAGAGGTGAAGAGCAATCACAGTGTGAAGAGCAATCACAGTGTGA 472  
DB 365 AGTGTGAACCCCTGAAGAGGTGAAGAGCAATCACAGTGTGAAGAGCAATCACAGTGTGA 424  
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DB 425 ATGATGACGCTGTCTCTATGTTGGAATTTGTTTCAATAAATTTCTCCCAATAAGCTTT 484  
QY 533 ACAGCTTCTGCAAG 560  
DB 485 ACAGCTTCTGCAAG 512

## RESULT 11

AF055474  
LOCUS AF055474 526 bp mRNA linear PRI 01-MAY-2000  
DEFINITION Homo sapiens GAGE-7B mRNA, complete cds.  
ACCESSION AF055474  
VERSION AF055474.1 GI:3511024  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 526)  
AUTHORS De Backer, O., Arden, K.C., Boretti, M., Vantomme, V., De Smet, C., Czekey, S., Viars, C.S., De Plaen, E., Brasseur, F., Chomez, P., Van den Eynde, B., Boon, T. and van der Bruggen, P.  
TITLE Characterization of the GAGE genes that are expressed in various human cancers and in normal testis  
JOURNAL Cancer Res. 59 (13), 3157-3165 (1999)  
MEDLINE 99323388  
PUBMED 10397259  
REFERENCE 2 (bases 1 to 526)  
AUTHORS De Backer, O.R.Y.  
TITLE Direct Submission  
JOURNAL Submitted (24-MAR-1998) Ludwig Institute for Cancer Research, Brussels Branch, 74 av. Hippocrate, Brussels B-1200, Belgium  
FEATURES  
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1. .526  
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/protein\_id="AAC33677.1"  
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/translation="MSWRGRSTYWPFRPRYVQPEPMRPEQFSDVEVPAPEEG  
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Query Match

79.1%; Score 443.2; DB 9; Length 526;



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Best Local Similarity 99.3%; Pred. No. 4.9e-106;
Matches 445; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 GAGGAAATCGACCTATTATTGGCCCTAGACCAAGCGCTATGTACAGCCTCCTGAAGTGA 172
Db 65 GAGGAAGATCGACCTATTATTGGCCCTAGACCAAGCGCTATGTACAGCCTCCTGAAGTGA 124
QY 173 TTGGGCTATGGCCCGCCGAGCTTCAGTGATGAAGTGAACCAACACCTGAAGAG 232
Db 125 TTGGGCTATGGCCCGCCGAGCTTCAGTGATGAAGTGAACCAACACCTGAAGAG 184
QY 233 GGGAAACCAAGCACTCAACCTCAGGATCCCTGAGCTCTCAGGAGGAGAGGAGGAG 292
Db 185 GGGAAACCAAGCACTCAACCTCAGGATCCCTGAGCTCTCAGGAGGAGAGGAGGAG 244
QY 293 CATCTGCAAGTCAAGGCGCCGAGCCTGGAAGCTGATGATCCAGGAAACAGGCTCACCCACAGA 352
Db 245 CATCTGCAAGTCAAGGCGCCGAGCCTGGAAGCTCATAGCCAGGAAACAGGCTCACCCACAGA 304
QY 353 CTGGGTGTGAGTGAAGATGTCCTGATGGGAGGAGATGACACCGCCCAATCCAGG 412
Db 305 CTGGGTGTGAGTGAAGATGTCCTGATGGGAGGAGATGACACCGCCCAATCCAGG 364
QY 413 AGGTGAAAACCGCTCAAGAGGTGAAAAGCAATCACAGTGTAAAAGAGGACAGCTTGAA 472
Db 365 AGGTGAAAACCGCTCAAGAGGTGAAAAGCAATCACAGTGTAAAAGAGGACAGCTTGAA 424
QY 473 ATGATGCAAGCTGCTCCTATGTTGGAATTTGTTTCAATTAATTTCCCAATAAAGCTTT 532
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QY 533 ACAGCCTTCTGCAAGAGAAAAA 560
Db 485 ACAGCCTTCTGCAAGAGAAAAA 512

RESULT 12
LOCUS AR028490
DEFINITION Sequence 16 from patent US 5858689.
ACCESSION AR028490
VERSION AR028490.1 GI:5940463
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 540)
AUTHORS van der Bruggen,P., van den Eynde,B., DeBacker,O. and Boon-Falleur,T.
TITLE Isolated peptides derived from the gage tumor rejection antigen
JOURNAL Precursor and uses thereof
PATENT: US 5858689-A 16 12-JAN-1999;
FEATURES
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Location/Qualifiers
1..540
/organism="unknown"
/mol_type="unassigned DNA"

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Query Match 79.1%; Score 443.2; DB 6; Length 540;
Best Local Similarity 99.3%; Pred. No. 4.9e-106;
Matches 445; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 GAGGAAATCGACCTATTATTGGCCCTAGACCAAGCGCTATGTACAGCCTCCTGAAGTGA 172
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QY 173 TTGGGCTATGGCCCGCCGAGCTTCAGTGATGAAGTGAACCAACACCTGAAGAG 232
Db 153 TTGGGCTATGGCCCGCCGAGCTTCAGTGATGAAGTGAACCAACACCTGAAGAG 212
QY 233 GGGAAACCAAGCACTCAACCTCAGGATCCCTGAGCTCTCAGGAGGAGAGGAGGAG 292
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Matches 445; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 293 CATCTGCAAGTCAAGGCGCCGAGCCTGGAAGCTGATGATCCAGGAAACAGGCTCACCCACAGA 352
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Db 333 CTGGGTGTGAGTGAAGATGTCCTGATGGGAGGAGATGACACCGCCCAATCCAGG 392
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QY 533 ACAGCCTTCTGCAAGAGAAAAA 560
Db 513 ACAGCCTTCTGCAAGAGAAAAA 540

RESULT 13
LOCUS BD231799
DEFINITION Isolated polypeptides binding with HLA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof.
ACCESSION BD231799
VERSION BD231799.1 GI:33041569
KEYWORDS JP 2002509859-A/9.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 540)
AUTHORS Bruggen,P.V.D., Eynde,B.V.D., Debacker,O., and Falleur,T.B.
TITLE Isolated polypeptides binding with HLA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof
JOURNAL Patent: JP 2002509859-A 9 02-APR-2002;
COMMENT LUDWIG INSTITUTE FOR CANCER RESEARCH
OS Homo sapiens (human)
PN JP 2002509859-A/9
PD 02-APR-2002
PF 12-JAN-1999 JP 2000528586
PI 23-JAN-1998 US 09/012818
PI PIERRE VAN DER BRUGGEN,BENOIT VAN DEN EYNDE,OLIVIER DEBACKER, THIERRY BOON FALLEUR
PC C07K4/12,C12N15/09,C12P21/00,C12Q1/00,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
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Best Local Similarity 99.3%; Pred. No. 4.9e-106;
Matches 445; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 GAGGAAATCGACCTATTATTGGCCCTAGACCAAGCGCTATGTACAGCCTCCTGAAGTGA 172
Db 93 GAGGAAGATCGACCTATTATTGGCCCTAGACCAAGCGCTATGTACAGCCTCCTGAAGTGA 152
QY 173 TTGGGCTATGGCCCGCCGAGCTTCAGTGATGAAGTGAACCAACACCTGAAGAG 232
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Db 393 AGGTGAAACGCTGAAGAGGTGAAAGCAATCACAGTGTAAAGAGGACAGGTTGAA 452
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Db 453 ATGATGAGGTGCTCTATGTTGAAATTTGTTTCATTAATTTCTCCCAATAGCTTT 512
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Qy 533 ACAGCTTCTGCAAGAAAAA 560
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Db 513 ACAGCTTCTGCAAGAAAAA 540
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RESULT 14
LOCUS I55853 540 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 16 from patent US 5648226.
ACCESSION I55853
VERSION I55853.1 GI:2476647
KEYWORDS
SOURCE Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 540)
AUTHORS Van den Eynde, B., DeBacker, O. and Boon-Falleur, T.
TITLE Isolated peptides derived from tumor rejection antigens, and their use
JOURNAL
Patent: US 5648226-A 16 15-JUL-1997;
FEATURES
Location/Qualifiers
source 1..540
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Query Match 79.1%; Score 443.2; DB 6; Length 540;
Best Local Similarity 99.3%; Pred. No. 4.9e-106;
Matches 445; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 113 GAGGAAATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTCTGAAGTGA 172
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Db 513 ACAGCTTCTGCAAGAAAAA 540
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RESULT 15
LOCUS BD132469 540 bp DNA linear PAT 18-SEP-2002
DEFINITION Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof.
ACCESSION BD132469
VERSION BD132469.1 GI:23227414
KEYWORDS JP 2002507112-A/9.
SOURCE synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 540)
AUTHORS Debacker, O., Eynde, B. V. D. and Falleur, T. B.
TITLE Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof
JOURNAL Patent: JP 2002507112-A 9 05-MAR-2002;
LUDWIG INSTITUTE FOR CANCER RESEARCH
COMMENT PN JP 2002507112-A/9
PD 05-MAR-2002
PF 23-JUN-1997 JP 1998503430
PI 24-JUN-1996 US 08/669161
PI OLIVIER DEBACKER, BENOIT VAN DEN EYNDE, THIERRY BOON FALLEUR PC
A61K38/00, A61K45/05, C07K7/00, C07K14/82, C12N15/00 CC
Strandedness: Single;
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Best Local Similarity 99.3%; Pred. No. 4.9e-106;
Matches 445; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 113 GAGGAAATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTCTGAAGTGA 172
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Db 453 ATGATGCAGGCTGCTCCTATGTGTGGAATTTGTTGATTAAATTCCTCCCAATAAGCTTT 512  
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Search completed: August 8, 2004, 14:48:40  
Job time : 2563 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 8, 2004, 13:46:44 ; Search time 2815 Seconds

(without alignments)

5940.611 Million cell updates/sec

Title: US-09-782-745-15

Perfect score: 560

Sequence: 1 CTCATATTTCACACAGATGA.....CTGCAGAGAAAAA 560

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 30620086

Minimum DB seq length: 0

Maximum DB seq length: 560

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estnu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_hic:\*

9: gb\_estl:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estcom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_pbg:\*

27: em\_gss\_vrl:\*

28: gb\_gsl:\*

29: gb\_gsl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	441.2	78.8	537	12	EM832793
2	437	78.0	480	12	BG120336
3	434.8	77.6	521	13	BX108227
4	434.6	77.6	447	9	AI381509

C	5	433.6	77.4	457	10	AW510753
C	6	432	77.1	464	9	AA738037
	7	429.2	76.6	527	12	BI828605
	8	428.2	76.5	517	14	CF780547
C	9	423.8	75.7	489	9	AA447559
C	10	420	75.0	450	9	AA760996
C	11	407.4	72.7	418	9	AW016546
C	12	405.4	72.4	455	9	AI187350
C	13	404.6	72.2	509	12	BI868671
C	14	398.8	71.2	426	9	AA868226
C	15	374	66.8	505	14	CB115693
C	16	360.6	64.4	412	9	AW102587
C	17	353.2	63.1	383	12	EM836228
C	18	334	59.6	384	9	AA913206
	19	318.8	56.9	397	12	BG206349
	20	307.2	54.9	333	13	BUS33718
C	21	302.4	54.0	398	9	AA918604
	22	289.6	51.7	419	9	AA448542
	23	283.4	50.6	445	11	BC005363
	24	269.8	48.2	275	14	CB147043
	25	269.8	48.2	275	14	CB150355
	26	269.8	48.2	275	14	CB157288
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	28	245.4	43.8	383	13	BX283580
	29	242.4	43.3	341	12	BP431265
	30	231.8	41.4	258	12	BG186708
	31	226.6	40.5	253	12	BG184057
	32	223.4	39.9	261	12	BG199060
	33	221.6	39.6	245	12	BG212621
	34	216.6	38.7	292	12	BG212622
	35	215.2	38.4	320	12	BM836021
	36	213.2	38.1	245	12	BG208433
C	37	207.6	37.1	507	9	AA972716
C	38	206.4	36.9	224	9	AA738394
	39	205.4	36.7	256	12	BG216461
C	40	195.4	34.9	197	9	AI968311
C	41	192.8	34.4	226	12	BG220441
C	42	189.6	33.9	457	14	CF780497
C	43	173.6	31.0	280	14	X93834
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	45	172.2	30.8	520	14	CB961487

## ALIGNMENTS

RESULT 1	BM832793	537 bp	mRNA	linear	EST 06-MAR-2002
LOCUS	X-EST0107334	S5SNU484s1	Homo sapiens	CDNA clone	S5SNU484s1-8-F10
DEFINITION	5', mRNA sequence.				
ACCESSION	BM832793				
VERSION	BM832793.1	GI:19189202			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				

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        /lab_host="SNU-484"
        /clone_lib="SSNU484s1"
        /note="Organ: Stomach; Vector: pTZ19RP1; Site 1: EcoRI;
          Site 2: NotI; The poly (A)+ RNA was decapped with tobacco
          acid pyrophosphatase (TAP) and ligated with DNA-RNA linker
          including EcoRI site by treatment of T4 RNA ligase. The
          first strand cDNA was synthesized from oligo dt-selected
          mRNA by priming with dt-tailed vector. The dt-tailed
          vector was adjusted to have about 60nt. The cDNA vector
          was circularized with E. coli DNA ligase after digestion
          of EcoRI which site is also included in vector. An RNA
          strand converted to a DNA strand by Okayama-Berg method.
          The obtained cDNA vectors were used for transformation of
          competent cells E. coli Top10F' by electroporation method.
          After analyzing and sequencing about 2,000 ~ 3,000
          colonies in original cDNA library, the abundant cDNAs were
          selected and amplified by PCR reaction using vector region
          primer including T7 promoter as 5' primer and N(dT)14 as
          3' primer. The PCR products were used as template for
          synthesis of biotinylated single stranded RNA by in vitro
          transcription reaction. The synthesized RNA probes were
          hybridized with antisense single stranded cDNAs prepared
          from original library and incubated with avidin-gel.
          After removing DNA-RNA hybrids by centrifuge, the
          subtracted cDNA libraries were constructed by
          transformation of the remaining DNA into competent cells E.
          coli Top10F' with electroporation method."

  ORIGIN
    Query Match      78.8%; Score 441.2; DB 12; Length 537;
    Best Local Similarity 99.3%; Pred. No. 2.6e-87;
    Mismatches 0; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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  Qy 533 ACAGCCTTCTGAAAGAAAAA 558
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us-09-782-745-15.closed.rst

Db 512 ACAGCCTTCTGAAAGAAAAA 537

RESULT 2

BG120336 480 bp mRNA linear EST 30-JAN-2001

LOCUS 602353732F1 NIH\_MGC\_90 Homo sapiens cDNA clone IMAGE:4451958 5',

DEFINITION mRNA sequence.

ACCESSION BG120336

VERSION BG120336.1 GI:12613845

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Chiroptera; Hominidae; Homo.

REFERENCE 1 (bases 1 to 480)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>;

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [qgapbs-x@mail.nih.gov](mailto:qgapbs-x@mail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LUAM10239 row: p column: 07

High quality sequence stop: 480.

Location/Qualifiers

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/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4451958"

/tissue\_type="adenocarcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH MGC 90"

/note="Organ: liver; Vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 78.0%; Score 437; DB 12; Length 480;

Best Local Similarity 99.9%; Pred. No. 2.2e-86;

Mismatches 0; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 1 GAAATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTCTGAAGTGTG 60

Qy 176 GGCCTATGGGCCCGGAGCAGTTTCAGTGTATGAAGTGGAAACCGACACCTGGAAGAGGG 235

Db 61 GGCCTATGGGCCCGGAGCAGTTTCAGTGTATGAAGTGGAAACCGACACCTGGAAGAGGG 120

Qy 236 AACACGCAACTCAAGTCAGATCTCGAGTCTGCTCAGAGGGAGAGATGAGGAGCAT 295

Db 121 AACACGCAACTCAAGTCAGATCTCGAGTCTGCTCAGAGGGAGAGATGAGGAGCAT 180

Qy 296 CTGAGGTCAAGGGCCGAGGCTGAAGCTGTATAGCCAGGAAACAGGGTCACCCACAGATG 355

Db 181 CTGAGGTCAAGGGCCGAGGCTGAAGCTGTATAGCCAGGAAACAGGGTCACCCACAGATG 240

Qy 356 GGTGTGAGTGTGAAGATGGTCTGTATGGCGAGGAGATGGACCCGCCAAATCCAGAGG 415

Db 241 GGTGTGAGTGTGAAGATGGTCTGTATGGCGAGGAGATGGACCCGCCAAATCCAGAGG 300

Qy 416 TGAAGACGCTGGAAGAGGTGAAAGCAATCACTGTTTAAAGAAAGGACGTTGAAATG 475

Db 301 TGAAGACGCTGGAAGAGGTGAAAGCAATCACTGTTTAAAGAAAGGACGTTGAAATG 360

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QY 476 ATGAGGCTCCTATGTTGGAATTTCTTCAATTAATAATTCCTCCCAATAAAGCTTTTACA 535
Db 361 ATGAGGCTCCTATGTTGGAATTTCTTCAATTAATAATTCCTCCCAATAAAGCTTTTACA 420
QY 536 GCCTTCTGCAAAAGAAAAA 560
Db 421 GCCTTCTGCAAAAGAAAAA 445

RESULT 3
BX108227
LOCUS
DEFINITION
  BX108227 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE998K213161 ;
  IMAGE:1256204, mRNA sequence.
ACCESSION
  BX108227
VERSION
  BX108227.1 GI:27835080
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
  Radelof, U., Schneider, D. and Korn, B.
  Human Unigeneset - RZPD3
  Unpublished (2002)
  Contact: Ina Rolfs
  RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
  Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
  RZPD; IMAG998K213161.
  RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
  Human Unigeneset - RZPD3 (RZPDLIB No.972);
  http://www.rzpd.de/CloneCards/cgi-
  bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
  RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
  Heubnerweg 6, D-14059 Berlin, Germany
  Tel: +49 30 32639 101
  Fax: +49 30 32639 111
  www.rzpd.de
  This clone is available royalty-free from RZPD;
  contact RZPD (clone@rzpd.de) for further information. Seq primer:
  M13r, Primer sequence: TTTACACAGGAACACGCTAGAC.

FEATURES
  Location/Qualifiers
    1..521
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAG998K213161 ; IMAGE:1256204"
      /tissue_type="pooled germ cell tumors"
      /lab_host="DH10B"
      /clone_lib="NCI_CGAP GC3"
      /note="Vector: pT73D-Pac (Pharmacia) with a modified
      polylinker; 1st strand cDNA was prepared from 3 pooled
      germ cell tumors, and was then primed with a Not I -
      oligo(dT) primer. Double-stranded cDNA was ligated to Eco
      RI adaptors (Pharmacia), digested with Not I and cloned
      into the Not I and Eco RI sites of the modified pT73
      vector. Library is not normalized. Library was
      constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN
  Query Match 77.6%; Score 434.8; DB 13; Length 521;
  Best Local Similarity 98.4%; Pred. No. 6.8e-86;
  Matches 439; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 113 GAGGAAATCGACCTATTATTCGCTAGACCAAGCGCTATCTACAGCCTCTCTGAAGTGA 172
Db 75 GAGGAGATCGACCTGTTATTGGCTAGTCCCAAGCGCTATCTACAGCCTCTCTGAAGTGA 134
QY 173 TTGGGCTATGCGGCCCGGAGGCTTTCAGTGTGAAGTGAACACGACCACTGAAGAAG 232
Db 135 TTGGGCTATGCGGCCCGGAGGCTTTCAGTGTGAAGTGAACACGACCACTGAAGAAG 194

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QY 233 GGGAAACCGCACTCAACGTCAGGATCCTGCGAGCTGCTCAGAGGAGAGGATGAGGGAG 292
Db 195 GGGAAACCGCACTCAACGTCAGGATCCTGCGAGCTGCTCAGAGGAGAGGATGAGGGAG 254
QY 293 CATCTGCAAGTCAAGGGCGGAGCCTGAAGCTGATAGCCAGCAACAGGCTCACCCACAGA 352
Db 255 CATCTGCAAGTCAAGGGCGGAGCCTGAAGCTGATAGCCAGCAACAGGCTCACCCACAGA 314
QY 353 CTGGGTGTGAGTGTGAAGATGCTTCTGATGGCGAGGATGACCCGCCAAATCCAGAGG 412
Db 315 CTGGGTGTGAGTGTGAAGATGCTTCTGATGGCGAGGATGACCCGCCAAATCCAGAGG 374
QY 413 AGGTAAACCGCTCAAGAGAGGTGAAAAGCAATCAAGTGTAAAGAGGACGCTTGAA 472
Db 375 AGGTAAACCGCTCAAGAGAGGTGAAAAGCAATCAAGTGTAAAGAGGACGCTTGAA 434
QY 473 ATGATGCAAGGCTGCTCCTATGTTGGAATTTCTTCAATTAATAATTCCTCCCAATAAAGCTTT 532
Db 435 ATGATGCAAGGCTGCTCCTATGTTGGAATTTCTTCAATTAATAATTCCTCCCAATAAAGCTTT 494
QY 533 ACAGCCTTCTGCAAAAGAAAAA 558
Db 495 ACAGCCTTCTGCAAAAGAAAAA 520

RESULT 4
AI381509/c
LOCUS
DEFINITION
  AI381509.1 x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
  IMAGE:2092597 3' similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;
  mRNA sequence.
ACCESSION
  AI381509
VERSION
  AI381509.1 GI:4194290
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapsb@mail.nih.gov
  This clone is available royalty-free through LLNL ; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  Insert Length: 497 Std Error: 0.00
  Seq primer: -40UP from Gibco.

FEATURES
  Location/Qualifiers
    1..447
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:2092597"
      /lab_host="DH10B"
      /clone_lib="Soares NFL T GBC S1"
      /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
      a modified polylinker; Site 1: Not I; Site 2: Eco RI;
      Equal amounts of plasmid DNA from three normalized
      libraries (fetal lung NBHL19W, testis NHT, and B-cell
      NCI CGAP GCBI) were mixed, and ss circles were made in
      vitro. Following HAP purification, this DNA was used as
      tracer in a subtractive hybridization reaction. The driver
      was PCR-amplified cDNAs from pools of 5,000 clones made
      from the same 3 libraries. The pools consisted of
      I.M.A.G.E. clones 297480-302087, 682632-687239,
      726408-728711, and 729096-731399. Subtraction by Bento
      Soares and M. Fatima Bonaldo. "

ORIGIN
  Query Match 77.6%; Score 434.6; DB 9; Length 447;

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Best Local Similarity 99.1%; Pred. No. 7.5e-86; Mismatches 0; Indels 4; Gaps 0;
Matches 437; Conservative 0;

Qy 113 GAGAAATCGACCTATTATTGGCCCTAGACCAAGCGCTATGTACAGCTCCTCGAAGTGA 172
Db 441 GAGAAATCGACCTATTATTGGCCCTAGACCAAGCGCTATGTACAGCTCCTCGAAGTGA 382

Qy 173 TTGGGCTATGCGGCCCGAGCAGTTTCAGTGCATGAAGTGAACCAAGCAACACCTGAAGAAG 232
Db 381 TTGGGCTATGCGGCCCGAGCAGTTTCAGTGCATGAAGTGAACCAAGCAACACCTGAAGAAG 322

Qy 233 GGGAAACAGCAACTCAACGTCAGGATCCTCGAGCTCCTCAGGCGGAGAGATGAGGAG 292
Db 321 GGGAAACAGCAACTCAACGTCAGGATCCTCGAGCTCCTCAGGCGGAGAGATGAGGAG 262

Qy 293 CATCTGAGGTCAGGCGCGAGCCTGAAGCTGATAGCCAGGAAACAGGGGTCAACCCACAGA 352
Db 261 CATCTGAGGTCAGGCGCGAGCCTGAAGCTGATAGCCAGGAAACAGGGGTCAACCCACAGA 202

Qy 353 CTGGGTCGTGAGTGTGAAGATGGTCTCATGGGAGGAGATGGACCCGCCAAATCCAGAGG 412
Db 201 CTGGGTCGTGAGTGTGAAGATGGTCTCATGGGAGGAGATGGACCCGCCAAATCCAGAGG 142

Qy 413 AGGTGAAACCGCTGAAAGAGGTGAAAGCAATCACAGTGTATAAAGAGGCAAGCTTTGAA 472
Db 141 AGGTGAAACCGCTGAAAGAGGTGAAAGCAATCACAGTGTATAAAGAGGCAAGCTTTGAA 82

Qy 473 ATGATGAGGCTGCTCCTATGTTGGAATTTGTTTCAATAAATTTCTCCCAATAAGCTTT 532
Db 81 ATGATGAGGCTGCTCCTATGTTGGAATTTGTTTCAATAAATTTCTCCCAATAAGCTTT 22

Qy 533 ACAGCCTTCTGCAAGAAAAA 553
Db 21 ACAGCCTTCTGCAAGAAAAA 1

RESULT 5
AW510753/c
LOCUS
DEFINITION
h339D05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2911881 3' similar to SW:GGE4_HUMAN Q13068 GAGE-4 PROTEIN. ;,
mRNA sequence.
AW510753
VERSION
AW510753.1 GI:7148831
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 457)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
Location/Qualifiers
1. .457
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2911881"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pTY73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI-CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
```

```
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 77.4%; Score 433.6; DB 10; Length 457;
Best Local Similarity 99.1%; Pred. No. 1.3e-85;
Matches 436; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 113 GAGAAATCGACCTATTATTGGCCCTAGACCAAGCGCTATGTACAGCTCCTCGAAGTGA 172
Db 440 GAGAAATCGACCTATTATTGGCCCTAGACCAAGCGCTATGTACAGCTCCTCGAAGTGA 381

Qy 173 TTGGGCTATGCGGCCCGAGCAGTTTCAGTGCATGAAGTGAACCAAGCAACCTGAAGAAG 232
Db 380 TTGGGCTATGCGGCCCGAGCAGTTTCAGTGCATGAAGTGAACCAAGCAACCTGAAGAAG 321

Qy 233 GGGAAACAGCAACTCAACGTCAGGATCCTCGAGCTCCTCAGGCGGAGAGATGAGGAG 292
Db 320 GGGAAACAGCAACTCAACGTCAGGATCCTCGAGCTCCTCAGGCGGAGAGATGAGGAG 261

Qy 293 CATCTGAGGTCAGGCGCGAGCCTGAAGCTGATAGCCAGGAAACAGGGGTCAACCCACAGA 352
Db 260 CATCTGAGGTCAGGCGCGAGCCTGAAGCTGATAGCCAGGAAACAGGGGTCAACCCACAGA 201

Qy 353 CTGGGTCGTGAGTGTGAAGATGGTCTCATGGGAGGAGATGGACCCGCCAAATCCAGAGG 412
Db 200 CTGGGTCGTGAGTGTGAAGATGGTCTCATGGGAGGAGATGGACCCGCCAAATCCAGAGG 141

Qy 413 AGGTGAAACCGCTGAAAGAGGTGAAAGCAATCACAGTGTATAAAGAGGCAAGCTTTGAA 472
Db 140 AGGTGAAACCGCTGAAAGAGGTGAAAGCAATCACAGTGTATAAAGAGGCAAGCTTTGAA 81

Qy 473 ATGATGAGGCTGCTCCTATGTTGGAATTTGTTTCAATAAATTTCTCCCAATAAGCTTT 532
Db 80 ATGATGAGGCTGCTCCTATGTTGGAATTTGTTTCAATAAATTTCTCCCAATAAGCTTT 21

Qy 533 ACAGCCTTCTGCAAGAAAAA 552
Db 20 ACAGCCTTCTGCAAGAAAAA 1

RESULT 6
AA738037/c
LOCUS
DEFINITION
rx15e11.s1 NCI_CGAP GC3 Homo sapiens cDNA clone IMAGE:1256204 3'
similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;, mRNA sequence.
AA738037
ACCESSION
AA738037.1 GI:2768794
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 464)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Suck, M.D., Ph.D.
cDNA Library preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lemmon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert length: 511 Std Error: 0.00
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Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 435.  
Location/Qualifiers  
1. .464  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1256204"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP GC3"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from 3 pooled  
germ cell tumors, and was then primed with a Not I -  
oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified pT7T3  
vector. Library is not normalized. Library was  
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN  
Query Match 77.1%; Score 432; DB 9; Length 464;  
Best Local Similarity 97.8%; Pred. No. 2.8e-85;  
Matches 438; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
QY 113 GAGGAAATCGACCTATTATTGGCCCTAGACCAAGGCGCTATGTACAGCCTCTCTGAAGTGA 172  
Db 454 GAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGCGCTATGTACAGCCTCTCTGAAGTGA 395  
QY 173 TTGGGCTATGCGGCCGAGCGAGTTCAGTGTGAAGTGAAGCAACACCTGAAGAG 232  
Db 394 TTGGGCTATGCGGCCGAGCGAGTTCAGTGTGAAGTGAAGCAACACCTGAAGAG 335  
QY 233 GGGACCCAGCACTCAACCTCAGGATCTCGACGCTCTCAGAGGAGGAGTGAAGGAG 292  
Db 334 GGGACCCAGCACTCAACCTCAGGATCTCGACGCTCTCAGAGGAGGAGTGAAGGAG 275  
QY 293 CATCTGCAGGTCAAGGGCCGAGGCTGAAGCTGATAGCCAGGAACAGGCTCACCCACAGA 352  
Db 274 CATCTGCAGGTCAAGGGCCGAGGCTGAAGCTGATAGCCAGGAACAGGCTCACCCACAGA 215  
QY 353 CTGGGTGTGAAGTGTGAAGTGTCTCTGATGGGAGGAGTGAAGCCGCAAAATCCAGAG 412  
Db 214 CTGGGTGTGAAGTGTGAAGTGTCTCTGATGGGAGGAGTGAAGCCGCAAAATCCAGAG 155  
QY 413 AGGTGAAACGCTGAGAGAGTGAAGAGCAATCAGTGTAAAGAGGAGCAAGTTGAA 472  
Db 154 AGGTGAAACGCTGAGAGAGTGAAGAGCAATCAGTGTAAAGAGGAGCAAGTTGAA 95  
QY 473 ATGATGCAGGCTGCTCTATGTTGGAAATTTGTTTATTAAATTTCTCCCAATAAGATT 532  
Db 94 ATGATGCAGGCTGCTCTATGTTGGAAATTTGTTTATTAAATTTCTCCCAATAAGATT 35  
QY 533 ACAGCCTTCTGCAAGAAAAA 560  
Db 34 ACAGCCTTCTGCAAGAAAAA 7

RESULT 7  
B1826605  
LOCUS  
DEFINITION  
603077056F1 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5168892 5',  
mRNA sequence.  
ACCESSION B1826605.1 GI:15938155  
VERSION EST.  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1. (bases 1 to 527)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)  
Contact: Robert Scrausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM11419 row: p column: 13  
High quality sequence stop: 519.  
Location/Qualifiers  
1. .527  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5168892"  
/tissue\_type="medulla"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_119"  
/note="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: EcoRV (destroyed); RNA source normal medulla from  
anonymous male age 27. Library is oligo-dT primed and  
directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.3 kb, insert size range  
0.9-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 013. Note:  
this is a NIH\_MGC Library."

ORIGIN  
Query Match 76.6%; Score 429.2; DB 12; Length 527;  
Best Local Similarity 99.1%; Pred. No. 1.2e-84;  
Matches 442; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 113 GAGGAAATCGACCTATTATTGGCCCTAGACCAAGGCGCTATGTACAGCCTCTCTGAAGTGA 172  
Db 83 GAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGCGCTATGTACAGCCTCTCTGAAGTGA 142  
QY 173 TTGGGCTATGCGGCCGAGCGAGTTCAGTGTGAAGTGAAGCAACACCTGAAGAG 232  
Db 143 TTGGGCTATGCGGCCGAGCGAGTTCAGTGTGAAGTGAAGCAACACCTGAAGAG 202  
QY 233 GGGACCCAGCACTCAACCTCAGGATCTCGACGCTCTCAGAGGAGGAGTGAAGGAG 292  
Db 203 GGGACCCAGCACTCAACCTCAGGATCTCGACGCTCTCAGAGGAGGAGTGAAGGAG 262  
QY 293 CATCTGCAGGTCAAGGGCCGAGGCTGAAGCTGATAGCCAGGAACAGGCTCACCCACAGA 352  
Db 263 CATCTGCAGGTCAAGGGCCGAGGCTGAAGCTGATAGCCAGGAACAGGCTCACCCACAGA 322  
QY 353 CTGGGTGTGAAGTGTGAAGTGTCTCTGATGGGAGGAGTGAAGCCGCAAAATCCAGAG 412  
Db 323 CTGGGTGTGAAGTGTGAAGTGTCTCTGATGGGAGGAGTGAAGCCGCAAAATCCAGAG 382  
QY 413 AGGTGAAACGCTGAGAGAGTGAAGAGCAATCAGTGTAAAGAGGAGCAAGTTGAA 472  
Db 383 AGGTGAAACGCTGAGAGAGTGAAGAGCAATCAGTGTAAAGAGGAGCAAGTTGAA 442  
QY 473 ATGATGCAGGCTGCTCTATGTTGGAAATTTGTTTATTAAATTTCTCCCAATAAGCTTT 532  
Db 443 ATGATGCAGGCTGCTCTATGTTGGAAATTTGTTTATTAAATTTCTCCCAATAAGCTTT 502  
QY 533 ACAGCCTTCTGCAAGAAAAA 558  
Db 503 ACAGCCTTCTGCAAGAAAAA 527

RESULT 8  
CF780547  
LOCUS  
DEFINITION  
AGENCOURT\_15739102 NIH\_MGC\_217 Homo sapiens cDNA clone

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IMAGE:30524555 5', mRNA sequence.
CF780547 1 GI:37739989
EST.
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 517)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: gcapbs-x@mail.nih.gov
Tissue Procurement: James Martin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM604 row: e column: 12
High quality sequence stop: 517.
Location/Qualifiers
source
1. 517
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30524555"
/tissue_type="Pooled Chondrosarcoma Tumor cells"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_217"
/notes="Vector: pX-Asc; Site 1: EcoRI; Site 2: NotI;
Library is oligo-dT primed and directionally cloned.
Denatured RNA was size fractionated on a 1% agarose gel.
First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated with
EcoR I adaptor, digested with Not I and then cloned
directionally into pX-Asc vector. Average insert size
0.5-1kb. Adaptors 5' (AATTCGGCAGGAG)3' and 5'd
(CCTCGGCG)3'. 3' linker sequence - GCGCGCTCAGAGCC T18.
Sequencing primers 3' end: T3 promoter primer 5'd
(AATACCCCTCACTAAAGGGA)3'. 5' End: T7 promoter primer 5'd
(TAATACGACTCACTAGG)3'. Average insert size 0.5-1kb.
Library was constructed in the laboratory of M. Bento
Soares. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 76.5%; Score 428.2; DB 14; Length 517;
Best Local Similarity 99.3%; Pred. No. 2e-84;
Matches 430; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 113 GAGGAATTCAGCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCCTCGAAGTGA 172
Db 84 GAGGAATTCAGCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCCTCGAATGA 143

Qy 173 TTGGGCTATGCGGCCGAGCAGTTTCAGTGTAGTGAAGTGGAAACACCTGAAGAAG 232
Db 144 TTGGGCTATGCGGCCGAGCAGTTTCAGTGTAGTGAAGTGGAAACACCTGAAGAAG 203

Qy 233 GGGACCGGAACTCAAGCTCAGATCTGAGTCTCAGAGGGAGAGATGAGGAG 292
Db 204 GGGACCGGAACTCAAGCTCAGATCTGAGTCTCAGAGGGAGAGATGAGGAG 263

Qy 293 CATCTGAGGTCAAGGGCCGAGCTGAGTGTAGTGAAGTGGAAACACCTGACACAGA 352
Db 264 CATCTGAGGTCAAGGGCCGAGCTGAGTGTAGTGAAGTGGAAACACCTGACACAGA 323

Qy 353 CTGGGTGTGAGTGTGAAGTGTCTGTATGGGAGAGATGGACCCGCCAATCCAGAGG 412

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324 CTGGGTGTGAGTGTGAAGATGGTCTGATGGGAGAGATGGACCCCAATCCAGAGG 383
Qy 413 AGGTGAAACGCTGAGAAAGAGTGAAGCAATCACAGTGTAAAGAGGACGCTTGA 472
Db 384 AGGTGAAACGCTGAGAAAGAGTGAAGCAATCACAGTGTAAAGAGGACGCTTGA 443
Qy 473 ATGATGAGGCTCTCTCTATGTTGGAATTTGTTCAATAAATTTCTCCCAATAAGCTTT 532
Db 444 ATGATGAGGCTCTCTCTATGTTGGAATTTGTTCAATAAATTTCTCCCAATAAGCTTT 503
Qy 533 ACAGCCTTCTGCA 545
Db 504 ACAGCCTTCTGCA 516

RESULT 9
AA447559/c
LOCUS
DEFINITION
AA447559 489 bp mRNA linear EST 04-JUN-1997
zw81el1.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:782636
3' similar to TR:G914905 G914905 GAGE-4 PROTEIN. [1] ; mRNA
sequence.
ACCESSION
AA447559
VERSION
AA447559.1 GI:2161229
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 489)
REFERENCE
AUTHORS
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Scheilenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 427.
Location/Qualifiers
source
1. 489
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:782636"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis NHT"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5].
TGTTACCAATCTGAAGTGGGCGGCCCAATTTTTTTTTTTTTTTT 3' ].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 75.7%; Score 423.8; DB 9; Length 489;
Best Local Similarity 99.3%; Pred. No. 1.9e-83;
Matches 436; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Qy 113 GAGGAATTCAGCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCCTCGAAGTGA 172

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438 GAGGAAGATCGACCTATTATTGGCTTAGACCAAGCGCTATGTACAGCCTCTGAAGTGA 379  
173 TTGGGCTATGCGGCCGAGCAGTTCAGTGATGAAGTGAAGCAAGCAAGCAAGCAAG 232  
378 TT-GGCTATGCGGCCGAGCAGTTCAGTGATGAAGTGAAGCAAGCAAGCAAGCAAG 320  
233 GGGAAACAGCAACTCAACGTCAGAGTCTGACGCTCTCAGGAGGAGGAGGAGGAG 292  
319 GGGAAACAGCAACTCAACGTCAGAGTCTGACGCTCTCAGGAGGAGGAGGAGGAG 260  
293 CATCTCAGGTCAAGGCGCCGAGCCTGAAGCTGATAGCCAGGAAACAGGCTCACCCACAGA 352  
259 CATCTCAGGTCAAGGCGCCGAGCCTGAAGCTCATAGCCAGGAAACAGGCTCACCCACAGA 200  
353 CTGGGTGTCAGTGTGAAGTGTCTGATGCGGAGGAGATGACCCGCGCAATCCAGAGG 412  
199 CTGGGTGTCAGTGTGAAGTGTCTGATGCGGAGGAGATGACCCGCGCAATCCAGAGG 140  
413 AGGTGAAACCGCTGAAAGAGGTGAAAGCAATCACAGTGTAAAGAGGAGGAGGAGTGA 472  
139 AGGTGAAACCGCTGAAAGAGGTGAAAGCAATCACAGTGTAAAGAGGAGGAGGAGTGA 80  
473 ATGATGAGGCTGCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 532  
79 ATGATGAGGCTGCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 20  
533 ACAGCCTCTGCAAAAGAAA 551  
19 ACAGCCTCTGCAAAAGAAA 1

RESULT 10  
AA760996/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
AA760996 450 bp mRNA linear EST 26-JAN-1998  
similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ; mRNA sequence.  
AA760996  
AA760996.1 GI:2809926  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 450)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Seq primer: -40m3 fwd. ET from Amersham  
High quality sequence stop: 331.  
Location/Qualifiers  
1. 450  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="IMAGE:1257855"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI-CGAP GC4"  
/note="Vector: pYT3D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from 3 pooled  
germ cell tumors, and was then primed with a Not I -

oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified pYT3  
vector. Library is normalized. Library was constructed by  
Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 75.0%; Score 420; DB 9; Length 450;  
Best Local Similarity 98.4%; Pred. No. 1.3e-82;  
Matches 434; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 113 GAGGAAATCGACCTATTATTGGCTTAGACCAAGCGCTATGTACAGCCTCTGAAGTGA 172  
Db 440 GAGGAAATCGACCTATTATTGGCTTAGACCAAGCGCTATGTACAGCCTCTGAAGTGA 381  
QY 173 TTGGGCTATGCGGCCGAGCAGTTCAGTGATGAAGTGAAGCAAGCAAGCAAGCAAG 232  
Db 380 NTGTGCTATGCGGCCGAGCAGTTCAGTGATGAAGTGAAGCAAGCAAGCAAGCAAG 321  
QY 233 GGGAAACAGCAACTCAACGTCAGAGTCTGACGCTCTCAGGAGGAGGAGGAGGAG 292  
Db 320 GGGAAACAGCAACTCAACGTCAGAGTCTGACGCTCTCAGGAGGAGGAGGAGGAG 261  
QY 293 CATCTCAGGTCAAGGCGCCGAGCCTGAAGCTGATAGCCAGGAAACAGGCTCACCCACAGA 352  
Db 260 CATCTCAGGTCAAGGCGCCGAGCCTGAAGCTCATAGCCAGGAAACAGGCTCACCCACAGA 201  
QY 353 CTGGGTGTCAGTGTGAAGTGTCTGATGCGGAGGAGATGACCCGCGCAATCCAGAGG 412  
Db 200 CTGGGTGTCAGTGTGAAGTGTCTGATGCGGAGGAGATGACCCGCGCAATCCAGAGG 141  
QY 413 AGGTGAAACCGCTGAAAGAGGTGAAAGCAATCACAGTGTAAAGAGGAGGAGGAGTGA 472  
Db 140 AGGTGAAACCGCTGAAAGAGGTGAAAGCAATCACAGTGTAAAGAGGAGGAGGAGTGA 81  
QY 473 ATGATGAGGCTGCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 532  
Db 80 ATGATGAGGCTGCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 22  
QY 533 ACAGCCTCTGCAAAAGAAA 553  
Db 21 ACAGCCTCTGCAAAAGAAA 1

RESULT 11  
AA760996/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
AA760996 418 bp mRNA linear EST 10-SEP-1999  
UI-H-BIOP-abg-g-06-0-UI.s1 NCI-CGAP\_Sub2 Homo sapiens cDNA clone  
IMAGE:2711986 3, mRNA sequence.  
AA760996  
AA760996.1 GI:5965303  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 418)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:  
NCI-CGAP clone distribution information can be found through the  
I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Seq primer: M13 Forward  
POLYA=Yes.  
Location/Qualifiers

FEATURES

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2711986"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Sub2"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
NCI CGAP Sub2 library is a subtracted library derived from
BI. BI constitutes a mixture of 21 normalized or
subtracted NCI CGAP libraries: NCI CGAP Co4,
NCI CGAP Pr22, NCI CGAP P-28, NCI CGAP Co10,
NCI CGAP Co16, NCI CGAP Kid5, NCI CGAP Kid12,
NCI CGAP Kid3, NCI CGAP Kid11, NCI CGAP Lym2,
NCI CGAP Br2, NCI CGAP Co8, NCI CGAP CL11, NCI CGAP Lei2,
NCI CGAP Brn23, NCI CGAP Lu5, NCI CGAP Lu24,
NCI CGAP Brn23, NCI CGAP GC4, NCI CGAP GC6, NCI CGAP Brn25.
These 21 libraries were pooled and a single-stranded DNA
preparation of the resulting mixture was used as a tracer
in a subtractive hybridization with a driver whose
composition is detailed below: NCI CGAP Kid3 pool 1 LLAM
3334-3337, 3682-3683, 3798-3803 (IMAGE Clonoids
1322376-1323911, 1456008-1456775, 1500552-1502855)
NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778
(IMAGE Clonoids 1323912-1325831, 1471368-1472903,
1492104-1493255) NCI CGAP Lu5 pool 1 LLAM 3575-3582,
3851-3854 (IMAGE Clonoids 1414920-1417991,
1520904-1522439) NCI CGAP GC4 pool 1 LLAM 3164-3167,
3716-3720, 3733-3735 (IMAGE Clonoids 1257096-1258631,
1469064-1470983, 1475592-1476743) NCI CGAP Pr22 pool 1
LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonoids
985608-986759, 1101192-1101959, 1217928-1220615)
NCI CGAP Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE
Clonoids 1057416-1061255, 1144584-1145351) The resulting
subtracted library contained 4 million recombinants.
Subtraction was performed as previously described
[Bonaldo, Lennon & Soares (1996): Normalization and
Subtraction: Two Approaches To Facilitate Gene Discovery.
Genome Research 6, 791-806.
TAG_TISSUE=germ cell
TAG_LIB=NCI CGAP_GC4
TAG_SEQ=AAATC"

ORIGIN
Query Match 72.7%; Score 407.4; DB 9; Length 418;
Best Local Similarity 98.6%; Pred. No. 7.8e-80;
Matches 411; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 144 AAGGCGCTATGTACAGCTCTCTGAAGTGAATGGGCGCTATGGCGCCGAGCAGTTTCAGTGA 203
Db 418 AAGAGCGTACGTAGAGCTCTCTGAATGATTTGGGCGCTATGGCGCCGAGCAGTTTCAGTGA 359
Qy 204 TGAAGTGAACACGACCACTGAAGAGGGGAAACACGACACTCAACGTTCAGTTCCTGTC 263
Db 358 TGAAGTGAACACGACCACTGAAGAGGGGAAACACGACACTCAACGTTCAGTTCCTGTC 299
Qy 264 AGCTGCTCAGAGGGAGAGGATGAGGAGATCTGCAGTCAAGGGCGGAGCCTGGAAGC 323
Db 298 AGCTGCTCAGAGGGAGAGGATGAGGAGATCTGCAGTCAAGGGCGGAGCCTGGAAGC 239
Qy 324 TGATAGCCAGGAACAGGGGTACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTCTGATGG 383
Db 238 TCATAGCCAGGACAGGGTACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTCTGATGG 179
Qy 384 GCAGAGATGACCCGCAATTCAGAGAGGTGAACCGCTGAAGAGGTGAAGACA 443
Db 178 GCAGAGATGACCCGCAATTCAGAGAGGTGAACCGCTGAAGAGGTGAAGACA 119
Qy 444 ATCAGAGTGAAGAGGACGTTGAAGTATGATGACGGCTGCTCCTATGTTGGAATTT 503
Db 118 ATCAGAGTGAAGAGGACGTTGAAGTATGATGACGGCTGCTCCTATGTTGGAATTT 59
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504 GTTCATTAAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAGAAAGAAAAA 560
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58 GTTCATTAAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAGAAAGAAAAA 2
|||||

Al187350 455 bp mRNA linear EST 10-NOV-1998
qf29a05.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1751408
3' similar to SW:GGE4_HUMAN Q13068 GAGE-4 PROTEIN. [1] ; mRNA
sequence.
Al187350
Al187350.1 GI:3737988
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 455)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
TITLE Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapsb@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 504 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 391.
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/organism="Homo sapiens"
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/clone="IMAGE:1751408"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis NHT"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5].
TGTACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTTTTTT 3'.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization to Cot5 and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 72.4%; Score 405.4; DB 9; Length 455;
Best Local Similarity 97.1%; Pred. No. 2.2e-79;
Matches 434; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

Qy 113 GAGGAAATCGACCTATTATTGGCCTAGACCAAGCGCTATGTACAGCTCTCTGAAGTGA 172
Db 445 GAGGAAATCGACCTATTATTGGCCTAGA-CAAGCGCTATGT-CAGCTCTCTGAATGA 388
Qy 173 TTGGGCTATCGGCCCGCAGCAGTTCAGTGTAGTGGACCGACACCTCAAGGAAG 232
Db 387 TTGGGCTATCGGCCCGCAGCAGTTCAGTGTAGTGGACCGACACCTCAAGGAAG 328
Qy 233 GGGAAACAGCAACTCAACGTTCAGGATCTCTGACGTCTCAGAGGGAGAGGATGAGGAG 292
Db 327 GGGAAACAGCAACTCAACGTTCAGGATCTCTGACGTCTCAGAGGGAGAGGATGAGGAG 268
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QY 293 CATCTGAGGTCAAGGCCCGAAGCCTGAAGCTGATACCCAGGAACAGGGTCACCCACAGA 352
Db 267 CATCTGAGGTCAAGGCCCGAAGCCTGAAGCTGATACCCAGGAACAGGGTCACCCACAGA 208
QY 353 CTGGGTGTGAGTGAAGATGGTCTCTGATGGCAGGAGATGGACCCGCCCAAAATCCAGAGG 412
Db 207 CTGGGTGTGAGTGAAGATGGTCTCTGATGGCAGGAGATGGACCCGCCCAAAATCCAGAGG 148
QY 413 AGGTGAAAACCGCTGAGAGAGGTGAAGAACCAATCACAGTGTATAAGAGGACGCTTGAA 472
Db 147 AGGTGAAAACCGCTGAGAGAGGTGAAGAACCAATCCCCAGTGTATAAGAGGACGCTTGAA 88
QY 473 ATGATGAGGCTGCTCTCTATGTTGGAAATTTGTTCAATTAATAATCTCCCAATAAGCTTT 532
Db 87 ATGATGAGGCTGCTCTCTATGTTGGAAATTTGTTCAATTAATAATCTCCCAATAAGCTTT 28
QY 533 ACAGCCTTCTGCAAAAGAAAAA 559
Db 27 CCAGCCTTCTGCAAAAGAAAAA 1

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RESULT 13
LOCUS BI868671
DEFINITION 60392594F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5402663 5',
mRNA sequence.

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ACCESSION BI868671
VERSION BI868671.1 GI:16042344
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL2026 row: 1 column: 24
High quality sequence stop: 509.
Location/Qualifiers
1. .509
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5402663"
/tissue type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_90"
(note="Organ: liver; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 Kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library.")

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## FEATURES

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source
1. .509
Location/Qualifiers
1. .509
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5402663"
/tissue type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_90"
(note="Organ: liver; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 Kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library.")

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## ORIGIN

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Query Match 72.2%; Score 404.6; DB 12; Length 509;
Best Local Similarity 99.0%; Pred. No. 3.3e-79;
Matches 407; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 113 GAGGAAATCGACCTATTATTCGCTAGACCAAGCGCTATGACAGCTCTCTGAAGTGA 172
Db 99 GAGGAAATCGACCTATTATTCGCTAGACCAAGCGCTATGACAGCTCTCTGAAGTGA 158
QY 173 TTGGGCTATGCGGCCCGAGCAGTTCAGTGATGAAGTGAACACAGCAACACCTGAAGAG 232

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Db 159 TTGGGCTATGCGGCCCGAGCAGTTCAGTGATGAAGTGAACACAGCAACCTGAAGAG 218
QY 233 GGAACACAGCAACTCAACGTCAGGATCCTGACGCTGCTCAGGAGGAGAGGATGAGGAG 292
Db 219 GGAACACAGCAACTCAACGTCAGGATCCTGACGCTGCTCAGGAGGAGAGGATGAGGAG 278
QY 293 CATCTGAGGTCAAGGCCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCACAGA 352
Db 279 CATCTGAGGTCAAGGCCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCACAGA 338
QY 353 CTGGGTGTGAGTGAAGATGGTCTCTGATGGCAGGAGATGGACCCGCCCAAAATCCAGAGG 412
Db 339 CTGGGTGTGAGTGAAGATGGTCTCTGATGGCAGGAGATGGACCCGCCCAAAATCCAGAGG 398
QY 413 AGGTGAAAACCGCTGAGAGAGGTGAAGAACCAATCACAGTGTATAAGAGGACGCTTGAA 472
Db 399 AGGTGAAAACCGCTGAGAGAGGTGAAGAACCAATCACAGTGTATAAGAGGACGCTTGAA 458
QY 473 ATGATGAGGCTGCTCTCTATGTTGGAAATTTGTTCAATTAATAATCTCCCA 523
Db 459 ATGATGAGGCTGCTCTCTATGTTGGAAATTTGTTCAATTAATAATCTCCCA 509

```

## RESULT 14

```

AA868226/c
LOCUS AA868226
DEFINITION ak48h07.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1409245
3', similar to SW:GGE2_HUMAN Q13066 GAGE-2 PROTEIN. [1] ; mRNA
sequence.

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ACCESSION AA868226
VERSION AA868226.1 GI:2963671
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

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## FEATURES

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1. .426
Location/Qualifiers
1. .426
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1409245"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis NHT"
(note="Vector: pT7T3-Pac (Pharmacia) with a modified
polylinker; Site:1: Not I; Site:2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5]
TGTATCCAAATCTGAAGTGGAGCGGCCCAATTTTTTTTTTTT 3').
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library

```

went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "

/clone lib="L8SCK0"  
/note="Organ: Liver; Vector: pT73-Pac; Site 1: EcoRI; Site 2: NotI; The library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cell culture."

ORIGIN  
Query Match 71.2%; Score 398.8; DB 9; Length 426;  
Best Local Similarity 96.7%; Pred. No. 6.3e-78;  
Matches 406; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 130 TATGGCCTAGACCAAGCGCTATGTACAGCCCTCTGAAGTGTGGCCCTATGCGGCC 189  
Db 420 TATGGCCTAGACCAAGCGCTATGTACAGCCCTCTGAAGTGTGGCCCTATGCGGCC 361  
QY 190 GAGCAGTTCAGTGTAGTGAAGTGGACCAAGCAACCTCAAGAAAGGGGACAGCAACTCAA 249  
Db 360 GAGCAGTTCAGTGTAGTGAAGTGGACCAAGCAACCTCAAGAAAGGGGACAGCAACTCAA 301  
QY 250 CGTCAGGATCCTGACGTGCTCAGGAGGGAGAGGATGAGGAGCATCTGCAGGTCAGAGGG 309  
Db 300 CGTCAGGATCCTGACGTGCTCAGGAGGGAGAGGATGAGGAGCATCTGCAGGTCAGAGGG 241  
QY 310 CCGAAGCCTGAAGCTGATAGCCAGGACAGGCTCACCCACAGACTGGGTGTGAGTGTGA 369  
Db 240 CCGAAGCCTGAAGCTGATAGCCAGGACAGGCTCACCCACAGACTGGGTGTGAGTGTGA 181  
QY 370 GATGGTCTGATGGGACAGGATGACCCCGCAATCCAGAGGAGTGAACCGCTGAA 429  
Db 180 GATGGTCTGATGGGACAGGATGACCCCGCAATCCAGAGGAGTGAACCGCTGAA 121  
QY 430 GAAGGTGAAAGCAATCACAGTGTAAAGAGGACGCTTGAATGATGAGGCTGCTCC 489  
Db 120 GAAGGTGAAAGCAATCACAGTGTAAAGAGGACGCTTGAATGATGAGGCTGCTCC 61  
QY 490 TATGTTGGAATTTGTTCAATTAATTTCTCCCAATTAAGCTTACAGCTTCTCAAGA 549  
Db 60 TATGTTGGAATTTGTTCAATTAATTTCTCCCAATTAAGCTTACAGCTTCTCAAAA 1

RESULT 15  
CB115693  
LOCUS K-EST0159805 L8SCK0 Homo sapiens cdna clone L8SCK0-8-B09 5', mRNA  
DEFINITION K-EST0159805 L8SCK0 Homo sapiens cdna clone L8SCK0-8-B09 5', mRNA  
sequence.  
ACCESSION CB115693  
VERSION CB115693.1 GI:27941500  
KEYWORDS EST  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 505)  
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.  
TITLE 21C Frontier Korean EST Project 2001  
JOURNAL Unpublished (2002)  
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Email: yongsung@mail.kribb.re.kr  
Plate: 8 row: B column: 09  
High quality sequence stop: 505.

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1..505  
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Best Local Similarity 97.4%; Pred. No. 2e-72;  
Matches 380; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Db 81 GAGGAAAATCGACCTATTATTGGCCTAGACCAAGCGCTATGTACAGCCCTCTGGAAGTGA 140  
QY 173 TTGGGCTTATGCGGCCCGGAGCAGTTCTAGTGTGAAAGTGGAAACAGCAACCTGGAAGAAG 232  
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Db 321 CTGGGTGTAGTGTGAAGATGGTCTGATGGGAGGAGATGGACCCGCAATCCAGAGG 380  
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Search completed: August 8, 2004, 15:35:49  
Job time : 2818 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 8, 2004, 12:43:29 ; Search time 374 Seconds

(without alignments)  
6360.938 Million cell updates/sec

Title: US-09-782-745-15

Perfect score: 560

Sequence: 1 CTCATATTTTCACACAGATCA.....CTGCAAGAAAAA 560

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 5090240

Minimum DB seq length: 0

Maximum DB seq length: 560

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002s:\*

7: geneseqn2003as:\*

8: geneseqn2003bs:\*

9: geneseqn2003cs:\*

10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	560	100.0	560	2	AAX90520 GAGE-3 tu
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3	446.4	79.7	532	2	Aax90522 GAGE-5 tu
4	443.2	79.1	526	7	ADAI5802 Human GAG
5	443.2	79.1	540	2	Aax90521 GAGE-4 tu
6	441.6	78.9	540	2	AAX90523 GAGE-6 tu
7	438.4	78.3	532	2	Aav18720 cdna enco
8	432	77.1	539	2	Aav18721 cdna enco
9	431.8	77.1	528	6	ABL66323 Lung canc
10	430.8	76.9	528	7	ADAI5801 Human GAG
11	430.2	76.8	527	7	ACC51027 Human bla
12	430.2	76.8	527	7	ABX76236 Lung canc
13	429.2	76.6	538	2	AAX90519 GAGE-2 tu
14	425.8	76.0	541	2	Aav18719 cdna enco
15	421.2	75.2	530	7	ABZ20463 GAGE-2 fu
16	417.6	74.6	535	2	Aav18717 cdna enco
17	304.6	54.4	530	4	AAS60104 Human can
18	302.4	54.0	365	4	AAS60496 Human can
19	265.2	47.4	430	3	AAC02129 Human can
20	172.2	30.8	520	7	ABT15737 Human can
21	164.6	29.4	509	7	ABX77605 Different
22	164.6	29.4	509	8	ACD42232 Human GAG
23	164.6	29.4	509	9	Adc24646 Human CDN

## ALIGNMENTS

### RESULT 1

AAX90520

ID AAX90520 standard; cdNA; 560 BP.

XX AAX90520;

AC AAX90520;

DT 30-SEP-1999 (first entry)

XX GAGE-3 tumour rejection antigen clone nucleotide sequence.

XX Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection; therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;

XX Homo sapiens.

XX WO9937665-A1.

XX 29-JUL-1999.

XX 12-JAN-1999; 99WO-US000775.

XX 23-JAN-1998; 98US-00012818.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Falleur T; WPI; 1999-469111/39.

XX New isolated peptides which bind to HLA-A29 molecules, which are tumor rejection antigens used for detection and therapy of pathological conditions, e.g. cancer.

XX Example 13; Fig 4; 62pp; English.

XX The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic T lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present invention

XX Sequence 560 BP; 177 A; 119 C; 150 G; 114 T; 0 U; 0 Other;

24 155.4 27.8 503 5 AAS69484  
c 25 151.4 27.0 229 7 ABZ18686  
c 26 151.4 27.0 277 7 ABZ19551  
c 27 149.8 26.8 229 7 ABZ20497  
c 28 149.8 26.8 257 7 ABZ19955  
c 29 149.8 26.8 264 7 ABZ19755  
c 30 149.4 26.7 227 7 ABZ20480  
c 31 147.4 26.3 532 4 AAI60530  
c 32 137.4 24.5 225 7 ABZ19533  
c 33 137.4 24.5 259 7 ABZ19791  
c 34 132.2 23.6 528 7 ABT15728  
c 35 128.8 23.0 475 4 AAD14981  
c 36 123.8 22.1 538 7 ABT15736  
c 37 108 19.3 399 5 AAF68151  
c 38 108 19.3 399 6 ABK38062  
c 39 108 19.3 399 7 ACA10391  
c 40 108 19.3 399 7 ABX99342  
c 41 108 19.3 399 10 ADE72125  
c 42 103.6 18.5 505 6 AAD24228  
c 43 103.4 18.5 463 6 ABA92217  
c 44 101.6 18.1 515 4 AAH93807  
c 45 101.6 18.1 515 4 AAS63900

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ABZ18686 Group III  
ABZ19551 Group III  
ABZ20497 TFS1 subt  
ABZ19955 Group III  
ABZ19755 Group III  
ABZ20480 TFS1 subt  
AAI60530 Human pol  
ABZ19533 Group III  
ABZ19791 Group III  
ABT15728 Human can  
AAD14981 Human can  
ABT15736 Human can  
AAF68151 Human lun  
ABK38062 cDNA enco  
ACA10391 Human lun  
ABX99342 Lung canc  
ADE72125 Human lun  
AAD24228 Human dif  
ABA92217 Melanoma  
AAH93807 Human pro  
AAS63900 Human pro





Db 481 GGCTGCTCTCTATGTTGGAAATTTGTTCAATTAATAATTCCTCCAAATTAAGCTTTTACAGCCTT 540

QY 541 CTGCAAGAGAAAAA 560

Db 541 CTGCAAGAGAAAAA 560

RESULT 3

AAAG90522

ID AAX90522 standard; cDNA; 532 BP.

XX

AC AAX90522;

XX

DT 30-SEP-1999 (first entry)

XX

DE GAGE-5 tumour rejection antigen clone nucleotide sequence.

XX

KW Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection;

KW therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;

KW GAGE; ss.

XX

OS Homo sapiens.

XX

PN WO9937665-A1.

XX

PD 29-JUL-1999.

XX

PF 12-JAN-1999; 99WO-US000775.

XX

PR 23-JAN-1998; 98US-00012818.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Falleur T;

XX

DR WPI; 1999-469111/39.

XX

PT New isolated peptides which bind to HLA-A29 molecules, which are tumor

PT rejection antigens used for detection and therapy of pathological

PT conditions, e.g. cancer.

XX

PS Example 13; Fig 4; 63pp; English.

XX

CC The present invention describes peptides which bind to human leukocyte

CC antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into

CC tumour rejection antigens. They can be used for detecting cytolytic T

CC lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-

CC typing assays. Complexes of HLA-29 molecules and the peptides can be used

CC for stimulating CTLs in vivo. The present sequence represents a GAGE

CC tumour rejection antigen clone, from an example from the present

CC invention

XX

SQ Sequence 532 BP; 156 A; 111 C; 154 G; 111 T; 0 U; 0 Other;

Query Match 79.7%; Score 446.4; DB 2; Length 532;

Best Local Similarity 99.8%; Pred. No. 2.3e-118;

Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 113 GAGGAATTCGACCTATTATTGGCTAGACACAGGCGTATGTACAGCCTCTGAAGTGA 172

Db 85 GAGGAAGATCGACCTATTATTGGCTAGACACAGGCGTATGTACAGCCTCTGAAGTGA 144

QY 173 TTGGGCTATGGCCGAGCAGTTCAGTGTAGTGAACAGCACCTGAAGAG 232

Db 145 TTGGGCTATGGCCGAGCAGTTCAGTGTAGTGAACAGCACCTGAAGAG 204

QY 233 GGGAAACCAACTCAACGTTCAGGATCTCTGAGCTGCTCAGGAGGAGAGGATGAGGAG 292

Db 205 GGGAAACCAACTCAACGTTCAGGATCTCTGAGCTGCTCAGGAGGAGAGGATGAGGAG 264

QY 293 CATCTGCAGTCAAGGCCGAGCCTTGAAAGCTGTATGCCAGAAACAGGCTCACCCACAGA 352

Db 265 CATCTGCAGTCAAGGCCGAGCCTTGAAAGCTGTATGCCAGAAACAGGCTCACCCACAGA 324

QY 353 CTGGGTGTGAGTGTGAAGATGGTCTGTATGGGCGAGAGATGGACCGCCAAATCCAGAGG 412

Db 325 CTGGGTGTGAGTGTGAAGATGGTCTGTATGGGCGAGAGATGGACCGCCAAATCCAGAGG 384

QY 413 AGGTGAAAACGGCTGAGAGAGGTGAAAAGCAATCAGAGTGTAAAGAGAGCGAGCTTGAA 472

Db 385 AGGTGAAAACGGCTGAGAGAGGTGAAAAGCAATCAGAGTGTAAAGAGAGCGAGCTTGAA 444

QY 473 ATGATCAGGCTGCTCTCTATGTTGGAAATTTGTTCAATTAATAATTCCTCCAAATTAAGCTTT 532

Db 445 ATGATCAGGCTGCTCTCTATGTTGGAAATTTGTTCAATTAATAATTCCTCCAAATTAAGCTTT 504

QY 533 ACAGCCTTCTGCAAGAGAAAAA 560

Db 505 ACAGCCTTCTGCAAGAGAAAAA 532

## RESULT 4

ADAL5802

ID ADAL5802 standard; cDNA; 526 BP.

XX

AC ADAL5802;

XX

DT 06-NOV-2003 (first entry)

XX

DE Human GAGE-7B cDNA.

XX

KW Human; GAGE-7B; gene; ss; cytolytic T lymphocyte; CTL;

KW human leukocyte antigen; HLA; tumour rejection antigen precursor;

KW major histocompatibility complex; MHC; cytolytic T cell proliferation;

KW chromosome Xp11.2-p11.4.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT 55..408

FT /\*tag= a

FT /product= "Human GAGE-7B"

FT /transl\_except= {pos:115..162, aa: GPMRPEQSGSDEVPENI}

FT /transl\_except= {pos:265..306, aa: HPQTGKPEAHSQBQ}

XX

PN US6509172-B1.

XX

PD 21-JAN-2003.

XX

PF 30-SEP-1998; 98US-00163748.

XX

PR 30-SEP-1998; 98US-00163748.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI De Backer O, Van Den Eynde B, Boon-Falleur T;

XX

DR WPI; 2003-401111/38.

XX

P-PSDB; ADAL5777.

XX

PT New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tumor

PT rejection antigen precursors, which complex to major histocompatibility

PT complex molecules to facilitate the proliferation of cytolytic T cells.

XX

PS Claim 1; Col 9-10; 15pp; English.

XX

CC The invention relates to isolated GAGE-7B and GAGE-8 polypeptides and the

CC nucleic acid molecules encoding them. The invention also relates to an

CC expression vector comprising an isolated nucleic acid molecule of the

CC invention operably linked to a promoter, a recombinant cell comprising

CC the isolated nucleic acid molecule or the expression vector and an

CC expression kit useful in generating cytolytic T lymphocytes (CTLs) or

CC determining if CTLs are present in a sample comprising the isolated

CC nucleic acid molecule and the isolated nucleic acid that encodes a human

CC leukocyte antigen (HLA) molecule. The GAGE-7B and GAGE-8 nucleic acid

CC molecules encode tumour rejection antigen precursors, which complex to

CC major histocompatibility complex (MHC) molecules to facilitate the  
 CC proliferation of cytolytic T cells. This sequence represents cDNA  
 CC encoding the human GAGE-7B polypeptide of the invention. The gene resides  
 CC on chromosome Xp11.2-p11.4.

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 XX  
 XX  
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 Best Local Similarity 99.3%; Pred. No. 1.9e-117;  
 Matches 445; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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 QY 173 TTGGGCTTATGCGGCCGAGAGTTCAGTGTGATGAAGTGGAAACCAAGCAACCTGAAGAAG 232  
 Db 125 TTGGGCTTATGCGGCCGAGAGTTCAGTGTGATGAAGTGGAAACCAAGCAACCTGAAGAAG 184  
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 QY 353 CTGGGTGTGAGTGTGAAGATGGTCTGTATGGGAGGAGATGAGCCGCAATCCAGG 412  
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 QY 413 AGGTGAAACCGCTGAAGAGGTGAAAGCAATCACAGTGTAAAGAGGACAGTTGAA 472  
 Db 365 AGGTGAAACCGCTGAAGAGGTGAAAGCAATCACAGTGTAAAGAGGACAGTTGAA 424  
 QY 473 ATGATGAGGCTGTCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 532  
 Db 425 ATGATGAGGCTGTCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 484  
 QY 533 ACAGCTTCTGCAAG 560  
 Db 485 ACAGCTTCTGCAAG 512

## RESULT 5

AAAX90521  
 ID AAAX90521 standard; cDNA; 540 BP.

XX  
 AC AAAX90521;

XX  
 DT 30-SEP-1999 (first entry)

XX  
 DE GAGE-4 tumour rejection antigen clone nucleotide sequence.

XX  
 KW Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection;  
 KW therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;  
 KW GAGE; ss.

XX  
 OS Homo sapiens.

XX  
 PN WO9937665-A1.

XX  
 PD 29-JUL-1999.

XX  
 PF 12-JAN-1999; 99WO-US000775.

XX  
 PR 23-JAN-1998; 98US-00012818.

XX  
 PA (LUDWIG) LUDWIG INST CANCER RES.

XX  
 PI Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Falleur T;

XX  
 DR WPI; 1999-469111/39.

XX  
 PT New isolated peptides which bind to HLA-A29 molecules, which are tumor  
 PT rejection antigens used for detection and therapy of pathological  
 PT conditions, e.g. cancer.

XX  
 PS Example 13; Fig 4; 62pp; English.

XX  
 XX  
 CC The present invention describes peptides which bind to human leukocyte  
 CC antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into  
 CC tumour rejection antigens. They can be used for detecting cytolytic T  
 CC lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-  
 CC typing assays. Complexes of HLA-29 molecules and the peptides can be used  
 CC for stimulating CTLs in vivo. The present sequence represents a GAGE  
 CC tumour rejection antigen clone, from an example from the present  
 CC invention

XX  
 SQ Sequence 540 BP; 159 A; 114 C; 156 G; 111 T; 0 U; 0 Other;

Query Match 79.1%; Score 443.2; DB 2; Length 540;  
 Best Local Similarity 99.3%; Pred. No. 1.9e-117;  
 Matches 445; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 GAGGAAATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTCTGAAGTGA 172

Db 93 GAGGAAATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTCTGAAGTGA 152

QY 173 TTGGGCTTATGCGGCCGAGAGTTCAGTGTGATGAAGTGGAAACCAAGCAACCTGAAGAAG 232

Db 153 TTGGGCTTATGCGGCCGAGAGTTCAGTGTGATGAAGTGGAAACCAAGCAACCTGAAGAAG 212

QY 233 GGGAAACAGCAACTCAACGTCAGGATCTGCGAGTCTGAGGAGGAGAGGATCAGGAG 292

Db 213 GGGAAACAGCAACTCAACGTCAGGATCTGCGAGTCTGAGGAGGAGAGGATCAGGAG 272

QY 293 CATCTGAGGTCAAGGGCCGAGGCTGAAGCTGTAGCTGATAGCCAGGAACAGGGTCAACCAAGA 352

Db 273 CATCTGAGGTCAAGGGCCGAGGCTGAAGCTGTAGCTGATAGCCAGGAACAGGGTCAACCAAGA 332

QY 353 CTGGGTGTGAGTGTGAAGATGGTCTGTATGGGAGGAGATGAGCCGCAATCCAGG 412

Db 333 CTGGGTGTGAGTGTGAAGATGGTCTGTATGGGAGGAGATGAGCCGCAATCCAGG 392

QY 413 AGGTGAAACCGCTGAAGAGGTGAAAGCAATCACAGTGTAAAGAGGACAGTTGAA 472

Db 393 AGGTGAAACCGCTGAAGAGGTGAAAGCAATCACAGTGTAAAGAGGACAGTTGAA 452

QY 473 ATGATGAGGCTGTCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 532

Db 453 ATGATGAGGCTGTCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 512

## RESULT 6

AAAX90523

ID AAAX90523 standard; cDNA; 540 BP.

XX  
 AC AAAX90523;

XX  
 DT 30-SEP-1999 (first entry)

XX  
 DE GAGE-6 tumour rejection antigen clone nucleotide sequence.

XX  
 KW Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection;  
 KW therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;  
 KW GAGE; ss.

XX  
 OS Homo sapiens.

XX  
 PN WO9937665-A1.

```
PD 29-JUL-1999.
XX
XX
XX 12-JAN-1999; 99WO-US000775.
XX
XX 23-JAN-1998; 98US-00012818.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Falleur T;
XX WPI; 1999-469111/39.
XX
XX New isolated peptides which bind to HLA-A29 molecules, which are tumor
XX rejection antigens used for detection and therapy of pathological
XX conditions, e.g. cancer.
XX
XX Example 13; Fig 4; 62pp; English.
XX
XX The present invention describes peptides which bind to human leukocyte
XX antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into
XX tumour rejection antigens. They can be used for detecting cytolytic T
XX lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-
XX typing assays. Complexes of HLA-A29 molecules and the peptides can be used
XX for stimulating CTLs in vivo. The present sequence represents a GAGE
XX tumour rejection antigen clone, from an example from the present
XX invention
XX
XX Sequence 540 BP; 159 A; 113 C; 157 G; 111 T; 0 U; 0 Other;
XX
XX Query Match 78.9%; Score 441.6; DB 2; Length 540;
XX Best Local Similarity 99.1%; Pred. No. 5.5e-117;
XX Matches 444; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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XX 113 GAGGAAATCGACCTATTATGGCCCTAGACCAAGCGCTGTGTACAGCTCTCTGAAGTGA 172
XX
XX 92 GAGGAAGATCGACCTATTATGGCCCTAGACCAAGCGCTGTGTACAGCTCTCTGAAGTGA 151
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XX 173 TTGGGCTATGGGCGCCGAGCGATTCAGTGTGAAGTGAACAGCAACACCTGAAGAG 232
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XX 152 TTGGGCTATGGGCGCCGAGCGATTCAGTGTGAAGTGAAGTGAAGTGAAGAG 211
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XX 233 GGAACCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 292
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XX 212 GGAACCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 271
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XX 293 CATCTGCAGTCAAGGCGCCGAGCGCTCAAGTGTGAAGTGAAGTGAAGTGAAGTGAAG 352
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XX 272 CATCTGCAGTCAAGGCGCCGAGCGCTCAAGTGTGAAGTGAAGTGAAGTGAAGTGAAG 331
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XX 353 CTGGGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGA 412
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XX 332 CTGGGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGA 391
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XX 413 AGGTGAACCGCTCAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGA 472
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XX 473 ATGATGCGAGTGTCTCTATGTGTGAAGTGTGTGAAGTGTGTGAAGTGTGTGAAGTGTGTGA 532
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XX
XX RESULT 7
XX AAV18720
XX ID AAV18720 standard; cdNA; 532 BP.
XX
XX AC AAV18720;
XX
XX 30-JUL-1998 (first entry)
```

```
XX
XX DE
XX
XX KW GAGE tumour rejection antigen precursor; TRAP; tumour; diagnosis;
XX melanoma; antigen; cytolytic T cell clone proliferation;
XX HLA-typing assay; ss.
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XX OS Homo sapiens.
XX
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XX
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XX
XX 31-DEC-1997.
XX
XX 23-JUN-1997; 97WO-US010850.
XX
XX 24-JUN-1996; 96US-00669161.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Debacker O, Van Den Eynde B, Boon-Falleur T;
XX
XX WPI; 1998-076905/07.
XX P-PSDB; AAW47602.
XX
XX Isolated nucleic acid encoding GAGE tumour rejection antigen precursor -
XX processed by HLA-Cw6 molecules into peptides, useful to diagnose
XX melanomas.
XX
XX Example 13; Fig 4; 60pp; English.
XX
XX The present sequence encodes a GAGE-5 tumour rejection antigen
XX precursor (TRAP). The protein is expressed in a number of tumours. In
XX contrast the only normal tissue which expresses GAGE TRAP protein is
XX testis. Several GAGE TRAPs have been identified (see AAV18717-21). The
XX major difference between these proteins and GAGE-1 (AAV05540) is the
XX absence of a stretch of 143 bases located at position 379 to 521 of the
XX GAGE-1 TRAP sequence. The rest of the sequences show mismatches at
XX various position, with the exception of GAGE-3 whose 5' end is totally
XX different from the other GAGE cDNAs for the first 112 bases. This region
XX of GAGE-3 cDNA contains a long repeat and a hairpin structure. The
XX antigens can be used to diagnose melanomas, characterised by expression
XX of a TRAP or presentation of a tumour rejection antigen. Antigens shed
XX into blood or urine can be observed and then used to confirm a diagnosis
XX of melanoma using cytolytic T cell clone proliferation methodologies.
XX Other uses for the processed peptides, include HLA-typing assays for,
XX e.g. skin graft or organ transplants
XX
XX Sequence 532 BP; 154 A; 110 C; 156 G; 112 T; 0 U; 0 Other;
```

```
Query Match 78.3%; Score 438.4; DB 2; Length 532;
Best Local Similarity 98.7%; Pred. No. 4.6e-116;
Matches 442; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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XX 113 GAGGAAATCGACCTATTATGGCCCTAGACCAAGCGCTGTGTACAGCTCTCTGAAGTGA 172
XX
XX 85 GAGGAAGATCGACCTATTATGGCCCTAGACCAAGCGCTGTGTACAGCTCTCTGAAGTGA 144
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XX 145 TTGGGCTATGGGCGCCGAGCGATTCAGTGTGAAGTGAAGTGAAGTGAAGTGAAG 204
XX
XX 233 GGAACCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 292
XX
XX 205 GGAACCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 264
XX
XX 293 CATCTGCAGTCAAGGCGCCGAGCGCTCAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGA 352
```

Db	265	CATCTGAGTCAAGGCGGAGCCCTGAAGCTGATAGCCAGGACACAGGCTCACCCACAGA	324
QY	353	CTGGGTGTAGTGTGAAGATGTCCTGATGGGAGAGATGGACCCGCCAAATCCAGAGG	412
Db	325	CTGGGTGTAGTGTGAAGATGTCCTGATGGGAGGATGGACCCGCCAAATCCAGAGG	384
QY	413	AGGTGAAGACGCTGAGAGAGGTGAAGCAATCACAGTGTAAAGAGGCGAGTTGAA	472
Db	385	AGGTGAAGACGCTGAGAGAGGTGAAGCAATCACAGTGTAAAGAGGCGAGTTGAA	444
QY	473	ATGATGAGGCTGCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAGCTTT	532
Db	445	ATGATGAGGCTGCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAGCTTT	504
QY	533	ACAGCCTTCTGCAAGAAAAA	560
Db	505	ACAGCCTTCTGCAAGAAAAA	532
RESULT 8			
AAV18721			
ID	AAV18721	standard; cDNA; 539 BP.	
XX			
AC	AAV18721;		
XX			
DT	30-JUL-1998	(first entry)	
DE			
XX			
XX			
XX			
KW			
KW			
KW			
KW			
XX			
OS			
XX			
FH			
FT			
FT			
FT			
FT			
FT			
XX			
FN			
XX			
PD			
PF			
XX			
PR			
XX			
PA			
XX			
PI			
XX			
DR			
XX			
PT			
PT			
PT			
XX			
PS			
XX			
CC			
CC			
CC			
CC			
CC			
CC			
CC			
CC			
CC			
CC			
CC			
CC			

antigens can be used to diagnose melanomas, characterised by expression of a TRAP or presentation of a tumour rejection antigen. Antigens shed into blood or urine can be observed and then used to confirm a diagnosis of melanoma using cytolytic T cell clone proliferation methodologies. Other uses for the processed peptides, include HLA-typing assays for, e.g. skin graft or organ transplants

Sequence 539 BP; 157 A; 114 C; 157 G; 111 T; 0 U; 0 Other;

Query Match 77.1%; Score 432; DB 2; Length 539;

Best Local Similarity 97.8%; Pred. No. 3.3e-114;

Matches 438; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 113 GAGGAAATCGACTATTATTGGCTAGACCAAGGCGCTATGTACAGCTCTCTGAAGTGA 172

Db 92 GAGGAGATCGACTATTATTGGCTAGACCAAGGCGCTATGTACAGCTCTCTGAAGTGA 151

QY 173 TTGGGCTATGCGGCGGAGCAGTTTCAGTGTGAAGTGAACCAAGCAACCTGGAAGAG 232

Db 152 TTGGGCTATGCGGCGGAGCAGTTTCAGTGTGAAGTGAACCAAGCAACCTGGAAGAG 211

QY 233 GGGAAACAGCACTCAACGTCAGGATCTCGAGTCTCAGGAGGAGAGGATCAGGAG 292

Db 212 GGGAAACAGCACTCAACGTCAGGATCTCGAGTCTCAGGAGGAGAGGATCAGGAG 271

QY 293 CATCTGAGTCAAGGCGGAGGCTGAAGCTGATAGCCAGGACACAGGTCACCCACAGA 352

Db 272 CATCTGAGTCAAGGCGGAGGCTGAAGCTGATAGCCAGGACACAGGTCACCCACAGA 331

QY 353 CTGGGTGTAGTGTGAAGATGTCCTGATGGGAGGAGATGGACCCGCCAAATCCAGAGG 412

Db 332 CTGGGTGTAGTGTGAAGATGTCCTGATGGGAGGAGATGGACCCGCCAAATCCAGAGG 391

QY 413 AGGTGAAGACGCTGAGAGAGGTGAAGCAATCACAGTGTAAAGAGGCGAGTTGAA 472

Db 392 AGGTGAAGACGCTGAGAGAGGTGAAGCAATCACAGTGTAAAGAGGCGAGTTGAA 451

QY 473 ATGATGAGGCTGCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 532

Db 452 ATGATGAGGCTGCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 511

QY 533 ACAGCCTTCTGCAAGAAAAA

560

Db 512 ACAGCCTTCTGCAAGAAAAA

539

RESULT 9

ABL66323

ID ABL66323 standard; DNA; 528 BP.

XX

AC ABL66323;

XX

DT 15-MAY-2002 (first entry)

XX

DE Lung cancer related gene sequence SEQ ID NO:4660.

XX

XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;

KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;

KW cycostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;

KW gene; ds.

XX

OS Homo sapiens.

XX

PN WO200194629-A2.

XX

PD 13-DEC-2001.

XX

PF 30-MAY-2001; 2001WO-US010838.

XX

PR 05-JUN-2000; 2000US-0209473P.

PR 05-JUN-2000; 2000US-0209531P.

PR 18-SEP-2000; 2000US-0233133P.

PR 18-SEP-2000; 2000US-0233617F.

PR 20-SEP-2000; 2000US-0234009P.  
 PR 20-SEP-2000; 2000US-0234034P.  
 PR 20-SEP-2000; 2000US-0234052P.  
 PR 22-SEP-2000; 2000US-0234509P.  
 PR 22-SEP-2000; 2000US-0234567P.  
 PR 25-SEP-2000; 2000US-0234923P.  
 PR 25-SEP-2000; 2000US-0234924P.  
 PR 25-SEP-2000; 2000US-0235077P.  
 PR 25-SEP-2000; 2000US-0235082P.  
 PR 25-SEP-2000; 2000US-0235134P.  
 PR 25-SEP-2000; 2000US-0235280P.  
 PR 26-SEP-2000; 2000US-0235637P.  
 PR 26-SEP-2000; 2000US-0235638P.  
 PR 27-SEP-2000; 2000US-0235711P.  
 PR 27-SEP-2000; 2000US-0235720P.  
 PR 27-SEP-2000; 2000US-0235840P.  
 PR 28-SEP-2000; 2000US-0235863P.  
 PR 28-SEP-2000; 2000US-0236028P.  
 PR 28-SEP-2000; 2000US-0236032P.  
 PR 28-SEP-2000; 2000US-0236033P.  
 PR 28-SEP-2000; 2000US-0236034P.  
 PR 28-SEP-2000; 2000US-0236109P.  
 PR 28-SEP-2000; 2000US-0236111P.  
 PR 29-SEP-2000; 2000US-0236842P.  
 PR 29-SEP-2000; 2000US-0236891P.  
 PR 02-OCT-2000; 2000US-0237172P.  
 PR 02-OCT-2000; 2000US-0237173P.  
 PR 02-OCT-2000; 2000US-0237278P.  
 PR 02-OCT-2000; 2000US-0237294P.  
 PR 02-OCT-2000; 2000US-0237295P.  
 PR 03-OCT-2000; 2000US-0237316P.  
 PR 03-OCT-2000; 2000US-0237425P.  
 PR 03-OCT-2000; 2000US-0237598P.  
 PR 03-OCT-2000; 2000US-0237604P.  
 PR 03-OCT-2000; 2000US-0237606P.  
 PR 03-OCT-2000; 2000US-0237608P.  
 PR 01-NOV-2000; 2000US-0244867P.  
 PR 01-NOV-2000; 2000US-0245084P.  
 PA (AVAL-) AVALON PHARM.

XX Young PB, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;  
 PI Soppet DR, Weaver Z;  
 PI WPI; 2002-188264/24.

PT Screening for anti-neoplastic agent involves exposing cells to a chemical  
 PT agent to be tested for anti-neoplastic activity, and determining a change  
 PT in expression of a gene of a signature gene set.

XX Claim 1; SEQ ID NO 4660; 44pp; English.

XX The present invention describes a method (M1) for screening for an anti-  
 CC neoplastic agent. The method involves exposing cells to a chemical agent  
 CC to be tested for anti-neoplastic activity, determining a change in  
 CC expression of at least one gene (I) of a signature gene set, where (I)  
 CC comprises a sequence (S) selected from 8447 sequences (given in AB161664  
 CC to AB170110), or is at least 98% identical to (S), where a change in  
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic  
 CC activity and can be used in gene therapy. M1 can be used for screening an  
 CC anti-neoplastic agent, and can be used for producing a product which is  
 CC the data collected with respect to the anti-neoplastic agent as a result  
 CC of M1, and the data is sufficient to convey the chemical structure and/or  
 CC properties of the agent. M1 can be used in the treatment of cancer such  
 CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,  
 CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell  
 CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous  
 CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms'  
 CC tumour

XX Sequence 528 BP; 147 A; 114 C; 156 G; 111 T; 0 U; 0 Other;

XX Query Match

XX 77.1%; Score 431.8; DB 6; Length 528;

Best Local Similarity 99.5%; Pred. No. 3.7e-114;  
 Matches 433; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 113 GAGGAAATCGACCTATTATTGGCCCTAGACCAAGGCGCTATGACAGCCCTCCTGAAGTGA 172  
 DB |||||  
 QY 93 GAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGCGCTATGACAGCCCTCCTGAAGTGA 152  
 DB |||||  
 QY 173 TTGGGCTATGCGGCCCGAGCGATTTCAGTGATGAAGTGAACCCAGCAACACCTGAAGAAG 232  
 DB |||||  
 QY 153 TTGGGCTATGCGGCCCGAGCGATTTCAGTGATGAAGTGAACCCAGCAACACCTGAAGAAG 212  
 DB |||||  
 QY 233 GGGAAACCACTCAACCTCAGGATCCTGCGAGCTCTCAGGAGGAGAGGATCAGGGAG 292  
 DB |||||  
 QY 213 GGGAAACCACTCAACCTCAGGATCCTGCGAGCTCTCAGGAGGAGAGGATCAGGGAG 272  
 DB |||||  
 QY 293 CATCTGAGGTCAAGGGCCGAGCCCTGAAGCTGATAGCCAGCAACAGGGTCAACCCACAGA 352  
 DB |||||  
 QY 273 CATCTGAGGTCAAGGGCCGAGCCCTGAAGCTGATAGCCAGCAACAGGGTCAACCCACAGA 332  
 DB |||||  
 QY 353 CTGGGTGTGAGTGTGAAGATGCTCTGATGGCAGGAGATGACCCGCCAAATCCAGAGG 412  
 DB |||||  
 QY 333 CTGGGTGTGAGTGTGAAGATGCTCTGATGGCAGGAGATGACCCGCCAAATCCAGAGG 392  
 DB |||||  
 QY 413 AGGTGAAAACGCTGAAGAAGGTGAAGAAGCAATCAGTGTAAAGAGGACACCTTGA 472  
 DB |||||  
 QY 393 AGGTGAAAACGCTGAAGAAGGTGAAGAAGCAATCAGTGTAAAGAGGACACCTTGA 452  
 DB |||||  
 QY 473 ATGATGAGGCTGCTCTATGTTGGAATTTCTTCAATAAATTTCTCCCAATAAGCTTT 532  
 DB |||||  
 QY 453 ATGATGAGGCTGCTCTATGTTGGAATTTCTTCAATAAATTTCTCCCAATAAGCTTT 512  
 DB |||||  
 QY 533 ACAGCCTTCTGCAAA 547  
 DB |||||  
 QY 513 ACAGCCTTCTGCAAA 527  
 DB |||||

## RESULT 10

ADAL5801  
 ID ADAL5801 standard; cDNA; 528 BP.

XX ADAL5801;

XX 06-NOV-2003 (first entry)

XX Human GAGS-8 cDNA.

XX Human; GAGS-8; Gene; ss; cytolytic T lymphocyte; CTL;  
 KW human leukocyte antigen; HLA; tumour rejection antigen precursor;  
 KW major histocompatibility complex; MHC; cytolytic T cell proliferation;  
 KW Chromosome Xp11.2-p11.4.

XX Homo sapiens.

XX Key Location/Qualifiers  
 XX CDS 73..423

FT /\*tag= a  
 FT /product= "Human GAGS-8"  
 FT /transl\_except= (pos:244..246, aa:Gln)  
 FT /transl\_except= (pos:400..402, aa:Lys)

XX US6509172-B1.

XX 21-JAN-2003.

XX 30-SEP-1998; 98US-00163748.

XX 30-SEP-1998; 98US-00163748.

XX (LUDW-) LUDWIG INST CANCER RES.

XX De Backer O, Van Den Eynde B, Boon-Falleur T;

XX WPI; 2003-401119/38.

DR	P-PSDB; ADAL5778.
XX	
PT	New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tumor
PT	rejection antigen precursors, which complex to major histocompatibility
PT	complex molecules to facilitate the proliferation of cytolytic T cells.
XX	
XX	Claim 1; Col 7-10; 15pp; English.
PS	
XX	
CC	The invention relates to isolated GAGE-7B and GAGE-8 polypeptides and the
CC	nucleic acid molecules encoding them. The invention also relates to an
CC	expression vector comprising an isolated nucleic acid molecule of the
CC	invention operably linked to a promoter, a recombinant cell comprising
CC	the isolated nucleic acid molecule or the expression vector and an
CC	expression kit useful in generating cytolytic T lymphocytes (CTLs) or
CC	determining if CTLs are present in a sample comprising the isolated
CC	nucleic acid molecule and the isolated nucleic acid that encodes a human
CC	leukocyte antigen (HLA) molecule. The GAGE-7B and GAGE-8 nucleic acid
CC	molecules encode tumour rejection antigen precursors, which complex to
CC	major histocompatibility complex (MHC) molecules to facilitate the
CC	proliferation of cytolytic T cells. This sequence represents cDNA
CC	encoding the human GAGE-8 polypeptide of the invention. The gene resides
CC	on chromosome Xp11.2-p11.4.
XX	
SO	Sequence 528 BP; 158 A; 112 C; 151 G; 107 T; 0 U; 0 Other;
XX	

QY 413 AGGTGAAAACGGCTGAAGAGGTGAAAAGCAATCACAGTGTAAAGAGGACGTTGAA 472  
DB 392 AGGTGAAAACGGCTGAAGAGGTGAAAAGCAATCACAGTGTAAAGAGGACGTTGAA 451  
QY 473 ATGATGACGGCTGCTCTATGTTGGAAATTTGTTCAATTAATAATTCCTCCCAATAAGCTTT 532  
DB 452 ATGATGACGGCTGCTCTATGTTGGAAATTTGTTCAATTAATAATTCCTCCCAATAAGCTTT 511  
QY 533 ACAGCCTTCTGAAA 547  
DB 512 ACAGCCTTCTGAAA 526

RESULT 12  
ID ABX76236  
XX  
AC  
XX  
DT  
XX  
DE  
XX  
KW lung cancer-associated polynucleotide #105.  
KW lung cancer-associated polynucleotide; gene; ds; cytostratic; emphysema;  
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;  
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;  
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;  
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.  
OS Unidentified.  
XX  
XX WO200286443-A2.  
XX  
XX PD 31-OCT-2002.  
XX  
XX PF 18-APR-2002; 2002WO-US012476.  
XX  
XX PR 18-APR-2001; 2001US-0284770P.  
XX PR 10-MAY-2001; 2001US-0290492P.  
XX PR 09-NOV-2001; 2001US-0339245P.  
XX PR 13-NOV-2001; 2001US-0350666P.  
XX PR 29-NOV-2001; 2001US-0334370P.  
XX PR 12-APR-2002; 2002US-0372246P.  
XX  
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.  
XX  
XX PI Aziz N, Murray R;  
XX  
XX DR WPI; 2003-093161/08.  
XX  
XX P-PSDB; ABUS6512.  
XX  
XX PT Detecting a lung cancer-associated transcript in a cell from a patient  
XX for treating lung cancer, by contacting a biological sample from the  
XX patient with a polynucleotide that exhibits increased or decreased  
XX expression in lung cancer.  
XX  
XX PS Claim 22; Page 273; 453pp; English.  
XX

XX The invention relates to a method for detecting a lung cancer-associated  
XX transcript in a cell from a patient, comprising contacting a biological  
XX sample from the patient with a polynucleotide that selectively hybridises  
XX to a sequence that is at least 80 % identical to a gene that exhibits  
XX increased or decreased expression in lung cancer samples. Lung cancer-  
XX associated polynucleotides and polypeptides are used for identifying a  
XX compound that modulates a lung cancer-associated polypeptide, for  
XX inhibiting proliferation of a lung cancer-associated cell to treat lung  
XX cancer in a patient and for treating a mammal having lung cancer by  
XX administering a modulatory compound identified. The methods are useful  
XX for treating lung cancer, such as small cell lung cancer, non-small cell  
XX lung cancer or other benign or precancerous lesions, e.g. atelectasis,  
XX emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,  
XX hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and

CC bronchiectasis. The genes, polynucleotides and polypeptides are useful  
CC for diagnostic purposes and as targets for screening for therapeutic  
CC compounds that modulate lung cancer, such as antibodies. Sequences  
CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the  
CC invention  
XX  
SQ Sequence 527 BP; 146 A; 113 C; 157 G; 111 T; 0 U; 0 Other;  
Query Match 76.8%; Score 430.2; DB 7; Length 527;  
Best Local Similarity 99.3%; Pred. No. 1.1e-113;  
Matches 432; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 113 GAGGAAAATCGACCTATTATTGGCCTAGACCAAGCGCTATCTACAGCCTCTGAAGTGA 172  
DB 92 GAGGAAAGATCGACCTATTATTGGCCTAGACCAAGCGCTATCTACAGCCTCTGAAGTGA 151  
QY 173 TTGGCCCTATGCGCCCGAGCAGTTCAGTGTAGTGAAGTGAAGTGAAGTGAAGTGAAG 232  
DB 152 TTGGCCCTATGCGCCCGAGCAGTTCAGTGTAGTGAAGTGAAGTGAAGTGAAGTGAAG 211  
QY 233 GGGAAACCACTCAACGTCAGGATCCTGACAGTCTCAGGAGGAGGAGGAGGAGGAG 292  
DB 212 GGGAAACCACTCAACGTCAGGATCCTGACAGTCTCAGGAGGAGGAGGAGGAGGAG 271  
QY 293 CATCTGCAAGTCAAGGCGCGAAGCCTGAAGCTGTAGCCAGGAAACAGGTTCAACCCACAGA 352  
DB 272 CATCTGCAAGTCAAGGCGCGAAGCCTGAAGCTGTAGCCAGGAAACAGGTTCAACCCACAGA 331  
QY 353 CTGGGTGTGAGTGTGAAGATGCTCTGATGGCGAGGATGAGCCCGCAATCCAGAGG 412  
DB 332 CTGGGTGTGAGTGTGAAGATGCTCTGATGGCGAGGATGAGCCCGCAATCCAGAGG 391  
QY 413 AGGTGAAAACGCTGAAGAGGTGAAAAGCAATCACAGTGTAAAGAGGACACGTTGAA 472  
DB 392 AGGTGAAAACGCTGAAGAGGTGAAAAGCAATCACAGTGTAAAGAGGACACGTTGAA 451  
QY 473 ATGATGAGGCTGCTCCTATGTTGGAATTTGTTCAATTAATAATTCCTCCCAATAAGCTTT 532  
DB 452 ATGATGAGGCTGCTCCTATGTTGGAATTTGTTCAATTAATAATTCCTCCCAATAAGCTTT 511  
QY 533 ACAGCCTTCTGAAA 547  
DB 512 ACAGCCTTCTGAAA 526

RESULT 13  
AAAX90519  
ID AAAX90519 standard; cDNA; 538 BP.  
XX  
AC AAAX90519;  
XX  
DT 30-SEP-1999 (first entry)  
XX  
DE GAGE-2 tumour rejection antigen clone nucleotide sequence.  
XX  
KW Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection;  
KW therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;  
KW GAGE; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO9937665-A1.  
XX  
XX PD 29-JUL-1999.  
XX  
XX PF 12-JAN-1999; 99WO-US000775.  
XX  
XX PR 23-JAN-1998; 98US-00012818.  
XX  
XX PA (LUDW-) LUDWIG INST CANCER RES.  
XX  
XX PI Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Falleur T;  
XX

```
DR WPI; 1999-469111/39.
XX
XX New isolated peptides which bind to HLA-A29 molecules, which are tumor
PT rejection antigens used for detection and therapy of pathological
PT conditions, e.g. cancer.
XX
XX Example 13; Fig 4; 62pp; English.
XX
XX The present invention describes peptides which bind to human leukocyte
CC antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into
CC tumour rejection antigens. They can be used for detecting cytolytic T
CC lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-
CC typing assays. Complexes of HLA-29 molecules and the peptides can be used
CC for stimulating CTLs in vivo. The present sequence represents a GAGE
CC tumour rejection antigen clone, from an example from the present
CC invention
XX
XX Sequence 538 BP; 160 A; 116 C; 155 G; 107 T; 0 U; 0 Other;
SQ
Query Match 76.6%; Score 429.2; DB 2; Length 538;
Best Local Similarity 92.2%; Pred. No. 2.1e-113;
Matches 452; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 71 TCTTCTCGCCAACTCATATTTACACAGATGATCTCTCAGTAGAGGAAATCGACCTATT 130
Db 49 TCITTTTCTCTACTAGATTTCATCTGTGTGAAATATGAGTTGCGAGGAAGATCGACCT 108
QY 131 ATTGGCCTAGACCAAGCGGTATGTACAGCCTCTGAAAGTATGGCCCTATGGGCCCG 190
Db 109 ATGGCCCTAGACCAAGACGCTACGTAGAGCCTCTCTGAAATGATTTGGCCCTATGGGCCCG 168
QY 191 AGCAGTTTCAGTGTAGTGAAGTGAACCCAGCACACCTGAAAGAGGGAACCAAGCACTCAAC 250
Db 169 AGCAGTTTCAGTGTAGTGAAGTGAACCCAGCACACCTGAAAGAGGGAACCAAGCACTCAAC 228
QY 251 GTCAGGATCCTGCACTGCTCAGAGGAGGAGGATGAGGAGCATCTGCAGGTCAAGGGC 310
Db 229 GTCAGGATCCTGCACTGCTCAGAGGAGGAGGATGAGGAGCATCTGCAGGTCAAGGGC 288
QY 311 CGAAGCCTGAAGCTGTATGACGAGAACAGGGTCAACACAGACTGGGTGTGAGTGTGAAG 370
Db 289 CGAAGCCTGAAGCTCATAGCCAGGAACAGGGTCAACACAGACTGGGTGTGAGTGTGAAG 348
QY 371 ATGTCTCTGTGGGCGAGAGATGACCGCCAAATCCAGAGAGGAGTGAACACGCTCAAG 430
Db 349 ATGTCTCTGTGGGCGAGAGATGACCGCCAAATCCAGAGAGGAGTGAACACGCTCAAG 408
QY 431 AAGGTGAAAGCAATCAAGTGTGTTAAAGAGGAGGACCGTTGAAATGATGCGAGGTGCTCCT 490
Db 409 AAGGTGAAAGCAATCAAGTGTGTTAAAGAGGAGGACCGTTGAAATGATGCGAGGTGCTCCT 468
QY 491 ATGTTGGAATTTGTTCTTAAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAA 550
Db 469 ATGTTGGAATTTGTTCTTAAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAA 528
QY 551 AAAAAAAAAA 560
Db 529 AAAAAAAAAA 538
RESULT 14
AAV18719
ID AAV18719 standard; cDNA; 541 BP.
XX
XX AAV18719;
AC
XX
XX 30-JUL-1998 (first entry)
XX
XX cDNA encoding GAGE-4 tumour rejection antigen precursor.
XX
XX GAGE tumour rejection antigen precursor; TRAP; tumour; diagnosis;
KW melanoma; antigen; cytolytic T cell clone proliferation;
KW HLA-typing assay; ss.
```

```
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH CDS 83..435
FT /*tag= a
FT /transl_except= (pos:197..199, aa:Ala)
FT /transl_except= (pos:200..202, aa:Thr)
XX
XX WO9749417-A1.
XX
XX 31-DEC-1997.
XX
XX 23-JUN-1997; 97WO-US010850.
XX
XX 24-JUN-1996; 96US-00669161.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Debacker O, Van Den Eynde B, Boon-Falleur T;
XX
XX WPI; 1998-076905/07.
XX P-PSDB; AAW47601.
XX
XX Isolated nucleic acid encoding GAGE tumour rejection antigen precursor -
XX processed by HLA-Cw6 molecules into peptides, useful to diagnose
XX melanomas.
XX
XX Example 13; Fig 4; 60pp; English.
XX
XX The present sequence encodes a GAGE-4 tumour tumour rejection antigen
XX precursor (TRAP). The protein is expressed in a number of tumours. In
XX contrast the only normal tissue which expresses GAGE TRAP protein is
XX testis. Several GAGE TRAPs have been identified (see AAV18717-21). The
XX major difference between these proteins and GAGE-1 (AAV05540) is the
XX absence of a stretch of 143 bases located at position 379 to 521 of the
XX GAGE-1 TRAP sequence. The rest of the sequences show mismatches at
XX various position, with the exception of GAGE-3 whose 5' end is totally
XX different from the other GAGE cDNAs for the first 112 bases. This region
XX of GAGE-3 cDNA contains a long repeat and a hairpin structure. The
XX antigens can be used to diagnose melanomas, characterised by expression
XX of a TRAP or presentation of a tumour rejection antigen. Antigens shed
XX into blood or urine can be observed and then used to confirm a diagnosis
XX of melanoma using cytolytic T cell clone proliferation methodologies.
XX Other uses for the processed peptides, include HLA-typing assays for,
XX e.g. skin graft or organ transplants
XX
XX Sequence 541 BP; 158 A; 117 C; 154 G; 112 T; 0 U; 0 Other;
SQ
Query Match 76.0%; Score 425.8; DB 2; Length 541;
Best Local Similarity 98.2%; Pred. No. 2e-112;
Matches 441; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
QY 113 GAGAAATCGACCTATTATGGCTAGACCAAGCGCTATGTACAGCCTCTCAAGTGA 172
Db 93 GAGGAATCGACCTATTATTTGGCCTAGACCAAGCGCTATGTACAGCCTCTCAAAATGA 152
QY 173 TTGGGCTATGCGGCCCGAGCAGTTTCAGTGTATGAAGTGAACCAACACCTCAAGAG 232
Db 153 TTGGGCTATGCGGCCCGAGCAGTTTCAGTGTATGAAGTGAACCAACAGCCTCTCAAGAG 212
QY 233 GGGAACCAAGCAACTCAACGTCAGGATCCTGAGTGTCTCAGGAGGAGGATGAGGAG 292
Db 213 GGGAACCAAGCAACTCAACGTCAGGATCCTGAGTGTCTCAGGAGGAGGATGAGGAG 272
QY 293 CATCTGAGGTCAAGGGCCGAGCCTGAAGCTGTATGACGAGGAGGAGTCAACACAGA 352
Db 273 CATCTGAGGTCAAGGGCCGAGCCTGAAGCTGTATGACGAGGAGGAGTCAACACAGA 332
QY 353 CTGGGTGTGAGTGTGAAGATGCTCTCTGATGGGAGGAGATGAGCCGCAATCAAGG 412
Db 333 CTGGGTGTGAGTGTGAAGATGCTCTCTGATGGGAGGAGATGAGCCGCAATCAAGG 392
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QY 413 AGCTGAAAACCGCTGAAGAGGTGAAAAGCAATCACAGTGTCTTAAAGAGGACGCTTG-A 471
|
Db 393 AGCTGAAAACCGCTGAAGAGGTGAAAAGCAATCACAGTGTCTTAAAGAGGACGCTTGAA 452
|
QY 472 AATGATGCGAGGCTGCTCCTATGTTGAAAATTTGTTTCAATAAAATTTCTCCCAATAAAGCTT 531
|
Db 453 AATGATGCGAGGCTGCTCCTATGTTGAAAATTTGTTTCAATAAAATTTCTCCCAATAAAGCTT 512
|
QY 532 TACAGCCTTCTGCAAGAAAAA 560
|
Db 513 TACAGCCTTCTGCAAGAAAAA 541
|
RESULT 15
ABZ20463
ID ABZ20463 standard; cDNA; 530 BP.
XX
AC ABZ20463;
XX
DT 23-JAN-2003 (first entry)
XX
DE GAGE-2 full length cDNA sequence SEQ ID NO:2890.
XX
KW Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;
KW immune response; virology; immunology; microbiology; molecular biology;
KW recombinant DNA technology; gene; ss.
XX
OS Homo sapiens.
XX
FN WO200278516-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US010421.
XX
PR 30-MAR-2001; 2001US-0280255P.
XX
PR 28-AUG-2001; 2001US-0315563P.
XX
PR 09-JAN-2002; 2002US-0347313P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Wang S, Bangur CS, Gaiger A;
XX
DR WPI; 2003-058387/05.
XX
DR P-PSDB; ABP54447.
XX
PT New immunogenic polynucleotides or polypeptides useful for diagnosing,
PT preventing and treating cancer expressing CT or CP mRNA antigens, and in
PT virology, immunology, microbiology, molecular biology and recombinant DNA
PT techniques.
XX
PS Claim 1; SEQ ID NO 2890; 207pp; English.
XX
CC ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and
CC ABP54446 to ABP54472 represent protein (II) sequences, from the present
CC invention. (I) and (II) have cytosolic activity and can be used in gene
CC therapy and vaccines. (I), (II), antibodies and compositions from the
CC present invention are useful for diagnosing, preventing and treating
CC cancer, which expresses CT or CP mRNA antigens. They are useful for
CC stimulating immune response. They can also be useful in virology,
CC immunology, microbiology, molecular biology and recombinant DNA
CC techniques. N.B. The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
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SQ Sequence 530 BP; 152 A; 116 C; 155 G; 107 T; 0 U; 0 Other;
Query Match 75.2%; Score 421.2; DB 7; Length 530;
Best Local Similarity 92.1%; Pred.No. 4.2e-111;
Matches 444; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
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Job time : 376 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Maximum DB seq length: 540

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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

# SUMMARIES

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1	540	100.0	540	6	AR028490	AR028490 Sequence
2	540	100.0	540	6	BD231799	BD231799 Isolated
3	540	100.0	540	6	I55853	I55853 Sequence 16
4	540	100.0	540	6	BD132469	BD132469 Isolated,
5	534.2	98.9	539	6	AR028492	AR028492 Sequence
6	534.2	98.9	539	6	BD231801	BD231801 Isolated
7	534.2	98.9	539	6	I55855	I55855 Sequence 18
8	534.2	98.9	539	6	BD132471	BD132471 Isolated,
9	528.8	97.9	532	6	AR028491	AR028491 Sequence
10	528.8	97.9	532	6	BD231800	BD231800 Isolated
11	528.8	97.9	532	6	I55854	I55854 Sequence 17
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# ALIGNMENTS

RESULT 1  
LOCUS AR028490  
DEFINITION Sequence 16 from patent US 5858689.  
ACCESSION AR028490  
VERSION AR028490.1 GI:5940463  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 540)  
AUTHORS van den Bruggen,P., van den Eynde,B., DeBacker,O. and Boon-Fallieur,T.  
TITLE Isolated peptides derived from the gage tumor rejection antigen precursor and uses thereof

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JOURNAL Patent: US 5858689-A 16 12-JAN-1999;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2.8e-129; Indels 0; Gaps 0;  
Matches 540; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

BD231799 540 bp DNA linear PAT 17-JUL-2003  
LOCUS Isolated polypeptides binding with HLA-A29 molecule, nucleic acids  
DEFINITION as molecules encoding the same, and utilization thereof.  
ACCESSION BD231799.1 GI:33041569  
VERSION JP 2002509859-A/9.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 540)  
AUTHORS Bruggen, P.V.D., Bynde, B.V.D., DeBacker, O. and Falleur, T.B.  
TITLE Isolated polypeptides binding with HLA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof  
JOURNAL Patent: JP 2002509859-A 9 02-APR-2002;  
COMMENT LUDWIG INSTITUTE FOR CANCER RESEARCH  
OS Homo sapiens (human)  
PN JP 2002509859-A/9  
PD 02-APR-2002  
PF 12-JAN-1999 JP 2000528586  
PR 23-JAN-1998 US 09/012818  
PI PIERRE VAN DER BRUGEN, BENOIT VAN DEN EYNDE, OLIVIER DEBACKER, THIERRY BOON FALLEUR

PC C07K4/12, C12N15/09, C12P21/00, C12Q1/02, C12N15/00 CC  
Strandedness: Single;  
CC Topology: Linear;  
CC STRANDEDNESS:single, TOPOLOGY:linear  
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FT Location/Qualifiers  
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Query Match 100.0%; Score 540; DB 6; Length 540;  
Best Local Similarity 100.0%; Pred. No. 2.8e-129; Indels 0; Gaps 0;  
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RESULT 3

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LOCUS Sequence 16 from patent US 5648226.  
DEFINITION Isolated peptides derived from tumor rejection antigens, and their  
ACCESSION I55853  
VERSION I55853.1 GI:2476647  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 540)  
AUTHORS Van den Eynde, B., DeBacker, O. and Boon-Falleur, T.  
TITLE Isolated peptides derived from tumor rejection antigens, and their use  
JOURNAL Patent: US 5648226-A 16 15-JUL-1997;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2.8e-129;
Matches 540; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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LOCUS Isolated, nucleic acid molecules which code for GAGE tumor
DEFINITION rejection antigen, the tumor rejection antigen, and uses thereof.
ACCESSION BD132469
VERSION JP 2002507112-A/9,
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 540)
AUTHORS Debacher,O., Eynde,B.V.D. and Falleur,T.B.
TITLE Isolated, nucleic acid molecules which code for GAGE tumor
JOURNAL Isolated antigen, the tumor rejection antigen, and uses thereof
COMMENT Patent: JP 2002507112-A 9 05-MAR-2002;
LUDWIG INSTITUTE FOR CANCER RESEARCH
FN JP 2002507112-A/9
PD 05-MAR-2002
PR 23-JUN-1997 JP 1998503430
PF 24-JUN-1996 US 08/669161
PI OLIVIER DEBACKER,BENOIT VAN DEN EYNDE,THIERRY BOON FALLEUR PC
A61K38/00,A61K45/05,C07K7/00,C07K14/82,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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Matches 540; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS Sequence 18 from patent US 5858689.
DEFINITION AR028492
ACCESSION AR028492
VERSION AR028492.1 GI:5940465
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 539)
van der Bruggen,P., van den Eynde,B., DeBacker,O. and Boon-Falleur,T.
TITLE Isolated peptides derived from the gage tumor rejection antigen precursor and uses thereof
JOURNAL Patent: US 5858689-A 18 12-JAN-1999;
FEATURES Location/Qualifiers
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RESULT 6
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LOCUS Isolated polypeptides binding with HLA-A29 molecule, nucleic acids
DEFINITION as molecules encoding the same, and utilization thereof.
VERSION BD231801.1 GI:33041571
KEYWORDS JP 2002509859-A/11.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bruggen,P.V.D., Eynde,B.V.D., DeBacker,O. and Falleur,T.B.
AUTHORS Isolated polypeptides binding with HLA-A29 molecule, nucleic acids
TITLE as molecules encoding the same, and utilization thereof
JOURNAL Patent: JP 2002509859-A 11 02-APR-2002;
COMMENT LUDWIG INSTITUTE FOR CANCER RESEARCH
PN OS Homo sapiens (human)
PD JP 2002509859-A/11
PF 02-APR-2002
PI 12-JAN-1999 JP 2000528586
PI 23-JAN-1998 US 09/012818
PI PIERRE VAN DER BRUGGEN,BENOIT VAN DEN EYNDE,OLIVIER DEBACKER,
PI THIERRY BOON FALLEUR
PC C07K4/12,C12N15/09,C12P21/00,C12Q1/02,C12N15/00 CC
Strandedness: Single;
CC Topology: linear;
CC STRANDEDNESS:single,TOPOLOGY:linear
FH Key Location/Qualifiers
FT source 1..539
FT /organism='Homo sapiens'
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FEATURES
source
ORIGIN
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Query Match 98.9%; Score 534.2; DB 6; Length 539;
Best Local Similarity 99.4%; Pred. No. 8.9e-128;
Matches 536; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GCCAGGAGCTGTGAGGAGTGTGTGTCTTCCGCGTCCGACTCTTTTCTCTAC 61
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QY 62 TGAGATTCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTTAC 121
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QY 482 TTGTTCAATTAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAAATTAATTAATTAATTAATTA 540
Db 481 TTGTTCAATTAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAAATTAATTAATTAATTAATTA 539
RESULT 7
I55855 539 bp DNA linear PAT 07-OCT-1997
LOCUS Sequence 18 from patent US 5648226.
DEFINITION I55855
ACCESSION I55855
VERSION I55855.1 GI:2476649
KEYWORDS Unknown.
SOURCE Unclassified.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 539)
AUTHORS Van den Eynde B., DeBacker O. and Boon-Falleur, T.
TITLE Isolated peptides derived from tumor rejection antigens, and their use
JOURNAL Patent: US 5648226-A 18 15-JUL-1997;
FEATURES Location/Qualifiers
source 1..539
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ORIGIN
Query Match 98.9%; Score 534.2; DB 6; Length 539;
Best Local Similarity 99.4%; Pred. No. 8.9e-128;
Matches 536; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GCCAGGAGCTGTGAGGAGTGTGTGTCTTCCGCGTCCGACTCTTTTCTCTAC 61
Db 1 GCCAGGAGCTGTGAGGAGTGTGTGTCTTCCGCGTCCGACTCTTTTCTCTAC 60
QY 62 TGAGATTCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTTAC 121
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Db      61 TGAGATTTCATCTGTGTGAATAATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGA 120
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QY      182 GATGAAGTGGAAACAGCAACACCTGGAAGAGGGGAAACCACTCAACTCAAGTTCAGGATCCT 241
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QY      242 GCAGCTGTCTCAGAGGGAGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAGCCTGAA 301
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QY      302 GCTGATAGCCAGAAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGAT 361
Db      301 GCTGATAGCCAGAAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGAT 360
QY      362 GGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAACCGCTGAAAGAGTGAAGAAG 421
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QY      422 CAATCACAGTGTAAAGAGGACGCTTGAATGATGAGGTGCTCTCTATGTTGGAAT 481
Db      421 CAATCACAGTGTAAAGAGGACGCTTGAATGATGAGGTGCTCTCTATGTTGGAAT 480
QY      482 TTGTTTCATTAAATTTCTCCCAATAAGCTTTACAGCTTCTGCAAAAAAAGGCTGAA 540
Db      481 TTGTTTCATTAAATTTCTCCCAATAAGCTTTACAGCTTCTGCAAAAAAAGGCTGAA 539

RESULT 8
LOCUS      BD132471          539 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Isolated, nucleic acid molecules which code for GAGE tumor
ACCESSION  BD132471
VERSION    BD132471.1 GI:23227416
KEYWORDS   JP 2002507112-A/11.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 539)
AUTHORS   Debacker,O., Eynde,B.V.D. and Falleur,T.B.
TITLES    Isolated, nucleic acid molecules which code for GAGE tumor
          rejection antigen, the tumor rejection antigen, and uses thereof
JOURNAL    Patent: JP 2002507112-A 11 05-MAR-2002;
COMMENT    LUDWIG INSTITUTE FOR CANCER RESEARCH
          PN JP 2002507112-A/11
          PD 05-MAR-2002
          PF 23-JUN-1997 JP 1998503430
          PR 24-JUN-1996 US 08/669161
          PI OLIVIER DEBACKER,BENOIT VAN DEN EYNDE,THIERRY BOON FALLEUR PC
          A61K38/00,A61K45/05,C07K7/00,C07K14/82,C12N15/00 CC
Strandedness: Single;
CC Topology: linear;
FH Key Location/Qualifiers.
FEATURES   source
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ORIGIN
Query Match 98.9%; Score 534.2; DB 6; Length 539;
Best Local Similarity 99.4%; Pred. No. 8.9e-128;
Matches 536; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GCCAGGAGCTGTGAGGAGTGTCTGTGGTTCCTGCGCTCGGACTCTTTTCTCTCTAC 61
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QY      62 TGAGATTTCATCTGTGTGAATAATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGA 121

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Db      61 TGAGATTTCATCTGTGTGAATAATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGA 120
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QY      242 GCAGCTGTCTCAGAGGGAGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAGCCTGAA 301
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QY      302 GCTGATAGCCAGAAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGAT 361
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Db      361 GGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAACCGCTGAAAGAGTGAAGAAG 420
QY      422 CAATCACAGTGTAAAGAGGACGCTTGAATGATGAGGTGCTCTCTATGTTGGAAT 481
Db      421 CAATCACAGTGTAAAGAGGACGCTTGAATGATGAGGTGCTCTCTATGTTGGAAT 480
QY      482 TTGTTTCATTAAATTTCTCCCAATAAGCTTTACAGCTTCTGCAAAAAAAGGCTGAA 540
Db      481 TTGTTTCATTAAATTTCTCCCAATAAGCTTTACAGCTTCTGCAAAAAAAGGCTGAA 539

RESULT 9
LOCUS      AR028491          532 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 17 from patent US 5858689.
ACCESSION  AR028491
VERSION    AR028491.1 GI:5940464
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 532)
AUTHORS   van der Bruggen,P., van den Eynde,B., DeBacker,O. and
          Boon-Falleur,T.
TITLES    Isolated peptides derived from the gage tumor rejection antigen
          precursor and uses thereof
JOURNAL    Patent: US 5858689-A 17 12-JAN-1999;
FEATURES   Location/Qualifiers
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            1..532
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Query Match 97.9%; Score 528.8; DB 6; Length 532;
Best Local Similarity 99.6%; Pred. No. 2.2e-126;
Matches 530; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      9 AGCTGTGAGGAGTGTGTGTGTTCTGCGCTCGGACTCTTTTCTCTCTACTGAGATT 68
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QY      69 CATCTGTGTAATATGAGTTGGCGAGGAAGATCGACTATTATTGGCTAGACCAAGGC 128
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Db      121 GCTATGTACAGCTCTCTGAAATGATTTGGCCCTATGCGGCCCGAGCAGTTTCAAGTATGAAG 180
QY      189 TGGAAACAGCAACACCTGAAAGAGGGGAAACCAAGCAACTCAAGCTCAGATCTCAGCTG 248
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 QY 429 AGTGTGTTAAAGAGGACGTTGAAATGATGACAGCTGCTCTATGTTGGAAATTTGTTCA 488  
 Db 421 AGTGTGTTAAAGAGGACGTTGAAATGATGACAGCTGCTCTATGTTGGAAATTTGTTCA 480  
 QY 489 TTAATAATTTCCCAATAAAGCTTTTACAGCCTTCTGCAAAAAAAGAAAAA 540  
 Db 481 TTAATAATTTCCCAATAAAGCTTTTACAGCCTTCTGCAAAAAAAGAAAAA 532

RESULT 10  
 BD231800 532 bp DNA linear PAT 17-JUL-2003  
 LOCUS Isolated polypeptides binding with HLA-A29 molecule, nucleic acids  
 DEFINITION as molecules encoding the same, and utilization thereof.

ACCESSION BD231800.1 GI:33041570  
 VERSION JP 2002509859-A/10.  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 532)  
 AUTHORS Bruggen,P.V.D., Eynde,B.V.D., Debacker,O. and Faillur,T.B.  
 TITLE Isolated polypeptides binding with HLA-A29 molecule, nucleic acids  
 as molecules encoding the same, and utilization thereof  
 JOURNAL Patent: JP 2002509859-A 10 02-APR-2002;  
 LUDWIG INSTITUTE FOR CANCER RESEARCH

COMMENT OS Homo sapiens (human)  
 PN JP 2002509859-A/10  
 PD 02-APR-2002  
 PF 12-JAN-1999 JP 2000528586  
 PR 23-JAN-1998 US 09/012818  
 PI PIERRE VAN DER BRUGGEN,BENOIT VAN DEN EYNDE,OLIVIER DEBACKER,  
 PC C07K4/12,C12N15/09,C12P21/00,C12Q1/02,C12N15/00 CC  
 Strandedness: Single;  
 CC Topology: Linear;  
 CC STRANDEDNESS:single,TOPOLOGY:linear  
 FH Key Location/Qualifiers  
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 FT /organism='Homo sapiens (human)'.  
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ORIGIN  
 Query Match 97.9%; Score 528.8; DB 6; Length 532;  
 Best Local Similarity 99.6%; Pred. No. 2.2e-126;  
 Matches 530; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 AGCTGTGAGGAGTGTGTGGTCTCTGCGTCCGGACTCTTTTCTCTACTGAGATT 68  
 Db 1 AGCTGTGAGGAGTGTGTGGTCTCTGCGTCCGGACTCTTTTCTCTACTGAGATT 60  
 QY 69 CATCTGTGAAATATGATGTTGGCGAGGAGATCGACCTATTATTGGCCTAGACCAAGGC 128  
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QY 129 GCTATGTACAGCCTCTCTGAAATGATTGGGCTTATGGGCGCCGAGCAGTTCAGTGTGTAAG 188  
 Db 121 GCTATGTACAGCCTCTCTGAAATGATTGGGCTTATGGGCGCCGAGCAGTTCAGTGTGTAAG 180  
 QY 189 TGGAAACCAACACCTCTGAAGAGGGGAACCAAGCACTCAACGTCAAGATCTCTGACGCTG 248  
 Db 181 TGGAAACCAACACCTCTGAAGAGGGGAACCAAGCACTCAACGTCAAGATCTCTGACGCTG 240  
 QY 249 CTCAGGAGGAGGAGGATGAGGAGCATCTCGAGTCAAGGCGCGAAGCCCTGAAGCTGATA 308  
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 Db 361 AGATGACCGCGCCAAATCCAGAGAGGTGAAACCGCTGAAGAGGTGAAAGCAATCAC 420  
 QY 429 AGTGTGTTAAAGAGGACGTTGAAATGATGACAGCTGCTCTATGTTGGAAATTTGTTCA 488  
 Db 421 AGTGTGTTAAAGAGGACGTTGAAATGATGACAGCTGCTCTATGTTGGAAATTTGTTCA 480  
 QY 489 TTAATAATTTCCCAATAAAGCTTTTACAGCCTTCTGCAAAAAAAGAAAAA 540  
 Db 481 TTAATAATTTCCCAATAAAGCTTTTACAGCCTTCTGCAAAAAAAGAAAAA 532

RESULT 11  
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 LOCUS Sequence 17 from patent US 5648226.  
 DEFINITION 532 bp DNA linear PAT 07-OCT-1997  
 ACCESSION 155854  
 VERSION 155854.1 GI:2476648  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 532)  
 AUTHORS Van den Bynde,B., DeBacker,O. and Boon-Falleur,T.  
 TITLE Isolated peptides derived from tumor rejection antigens, and their use  
 JOURNAL Patent: US 5648226-A 17 15-JUL-1997;  
 FEATURES Location/Qualifiers  
 source 1..532  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

ORIGIN  
 Query Match 97.9%; Score 528.8; DB 6; Length 532;  
 Best Local Similarity 99.6%; Pred. No. 2.2e-126;  
 Matches 530; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 AGCTGTGAGGAGTGTGTGGTCTCTGCGTCCGGACTCTTTTCTCTACTGAGATT 68  
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 QY 69 CATCTGTGAAATATGATGTTGGCGAGGAGATCGACCTATTATTGGCCTAGACCAAGGC 128  
 Db 61 CATCTGTGAAATATGATGTTGGCGAGGAGATCGACCTATTATTGGCCTAGACCAAGGC 120  
 QY 129 GCTATGTACAGCCTCTCTGAAATGATTGGGCTTATGGGCGCCGAGCAGTTCAGTGTGTAAG 188  
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 QY 189 TGGAAACCAACACCTCTGAAGAGGGGAACCAAGCACTCAACGTCAAGATCTCTGACGCTG 248  
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Db 481 TTAATAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAAATAAAAAA 532

RESULT 12
BD132470 532 bp DNA linear PAT 18-SEP-2002
LOCUS Isolated, nucleic acid molecules which code for GAGE tumor
DEFINITION rejection antigen, the tumor rejection antigen, and uses thereof.
ACCESSION BD132470
VERSION JP 2002507112-A/10.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 532)
AUTHORS Debacter,O., Bynde,B.V.D. and Falleur,T.B.
TITILE Isolated, nucleic acid molecules which code for GAGE tumor
JOURNAL rejection antigen, the tumor rejection antigen, and uses thereof
PATENT: JP 2002507112-A 10 05-MAR-2002;
LUDWIG INSTITUTE FOR CANCER RESEARCH
COMMENT PN JP 2002507112-A/10
PD 05-MAR-2002
PF 23-JUN-1997 JP 1998503430
PR 24-JUN-1996 US 08/669161
PI OLIVIER DEBACKER,BENOIT VAN DEN EYNDE,THIERRY BOON FALLEUR PC
A61K38/00,A61K45/05,C07K7/00,C07K14/82,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
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/db_xref="taxon:32630"

ORIGIN
Query Match 97.9%; Score 528.8; DB 6; Length 532;
Best Local Similarity 99.6%; Pred. No. 2.2e-126;
Matches 530; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 AGCTGTGAGGAGTGTGTGGTTCCTCCGCTCCGAGTCTTTTCTCTACTCAGATT 68
Db 1 AGCTGTGAGGAGTGTGTGGTTCCTCCGCTCCGAGTCTTTTCTCTACTCAGATT 60
QY 69 CATCTGTGAAATATGATTGGCGAGGAAGATCGACCTATTTATTTGGCCTAGACCAAGGC 128
Db 61 CATCTGTGAAATATGATTGGCGAGGAAGATCGACCTATTTATTTGGCCTAGACCAAGGC 120
QY 129 GCTATGTACAGCTCCTGAAATGATTTGGCCCTATGGGCCCGAGCAGTTCACTGATGAAG 188
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Db 481 TTAATAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAAATAAAAAA 532

RESULT 13
AX334151 528 bp DNA linear PAT 09-JAN-2002
LOCUS Sequence 4660 from Patent WO0194629.
DEFINITION AX334151
ACCESSION AX334151
VERSION AX334151.1 GI:18124870
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horrigan,S., Soppet,D.R. and Weaver,Z.
TITILE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 4660 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
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ORIGIN
Query Match 97.8%; Score 528; DB 6; Length 528;
Best Local Similarity 100.0%; Pred. No. 3.6e-126;
Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCAGGAGCTGTGAGGAGTGTGTGGTTCCTGCGCTCGGACTCTTTTCTCTCTA 60
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Db 61 CTGAGATTCATCTGTGTAATATGAGTTGGCGAGGAAGATCGACTATTATTCGCTAG 120
QY 121 ACCAAGCGCTATGTACAGCCTCCTGAAATGATTGGGCTATGCGGCCCGAGCAGTTCA 180
Db 121 ACCAAGCGCTATGTACAGCCTCCTGAAATGATTGGGCTATGCGGCCCGAGCAGTTCA 180
QY 181 TGATGAAGTGAACACAGCAACACCTGAAGAGGGGAACCAAGCAACTCAAGTCAGGATCC 240
Db 181 TGATGAAGTGAAGCAGCAACACCTGAAGAGGGGAACCAAGCAACTCAAGTCAGGATCC 240
QY 241 TGCAGCTCTCTCAGGAGGAGGAGTGAAGGAGTCTGCAGGTCAAGGCCGGAAGCTTGA 300
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QY 481 TTTGTTCAATTAATAATCTCCCAATAAGCTTTACAGCCTTCTGCAAAA 528
Db 481 TTTGTTCAATTAATAATCTCCCAATAAGCTTTACAGCCTTCTGCAAAA 528

RESULT 14
HSU19145 528 bp mRNA linear PRI 04-DEC-1995
LOCUS Human GAGE-4 protein mRNA, complete cds.
DEFINITION U19145
ACCESSION U19145.1 GI:914904
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 528)
AUTHORS Van den Eynde,B., Peeters,O., De Backer,O., Gaugler,B., Lucas,S.
and Boon,T.
TITLE A new family of genes coding for an antigen recognized by
autologous cytolytic T lymphocytes on a human melanoma
J. Exp. Med. 182 (3), 689-698 (1995)
JOURNAL
MEDLINE 95378788
PUBMED 7544395
REFERENCE 2 (bases 1 to 528)
AUTHORS Van den Eynde,B.J.
TITLE Direct Submission
JOURNAL Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute
for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium
FEATURES
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CDS
Query Match 97.8%; Score 528; DB 9; Length 528;
Best Local Similarity 100.0%; Pred. No. 3.6e-126;
Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCAGGAGCTGTGAGGACGAGTGTGTGTGTCTGCGTCCGCGACTCTTTTCTCTTA 60
Db 1 CGCCAGGAGCTGTGAGGACGAGTGTGTGTGTCTGCGTCCGCGACTCTTTTCTCTTA 60
QY 61 CTGAGATTTCATCTGTGTGAATATGAGTTGGCGAGAGATGACCTATTATTGCCCTAG 120
Db 61 CTGAGATTTCATCTGTGTGAATATGAGTTGGCGAGAGATGACCTATTATTGCCCTAG 120
QY 121 ACCAAGGCGCTATGTACAGCCTCTGAAATGATGGGCTATGCGGCCCGAGCAGTTTCA 180
Db 121 ACCAAGGCGCTATGTACAGCCTCTGAAATGATGGGCTATGCGGCCCGAGCAGTTTCA 180
QY 181 TGATCAAGTGGAAACGACCAACCTGTAAGAGGGGAAACGACCACTCAACGTTCAGATCC 240
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Db 181 TGATCAAGTGGAAACGACCAACCTGTAAGAGGGGAAACGACCACTCAACGTTCAGATCC 240
QY 241 TGACAGCTGTCTCAGGAGGAGAGGATCAGGAGAGCATCTGCAGGTCAAGGGCCGAGCCTGA 300
Db 241 TGACAGCTGTCTCAGGAGGAGAGGATCAGGAGAGCATCTGCAGGTCAAGGGCCGAGCCTGA 300
QY 301 AGCTGATAGCCAGGAAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGA 360
Db 301 AGCTGATAGCCAGGAAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGA 360
QY 361 TGGGAGGAGATGACCCCGCAATTCAGAGGAGGTGAAACCCCTGAAGAGGTGAAA 420
Db 361 TGGGAGGAGATGACCCCGCAATTCAGAGGAGGTGAAACCCCTGAAGAGGTGAAA 420
QY 421 GCAATCACAGTGTAAAGAGGACCGTTGAAATGATGAGGCTGCTCTTATGTTGAAA 480
Db 421 GCAATCACAGTGTAAAGAGGACCGTTGAAATGATGAGGCTGCTCTTATGTTGAAA 480
QY 481 TTTGTTCAATTAATAATCTCCCAATAAGCTTTACAGCCTTCTGCAAAA 528
Db 481 TTTGTTCAATTAATAATCTCCCAATAAGCTTTACAGCCTTCTGCAAAA 528

RESULT 15
HSU19147 527 bp mRNA linear PRI 04-DEC-1995
LOCUS Human GAGE-6 protein mRNA, complete cds.
DEFINITION U19147
ACCESSION U19147.1 GI:914908
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 527)
AUTHORS Van den Eynde,B., Peeters,O., De Backer,O., Gaugler,B., Lucas,S.
and Boon,T.
TITLE A new family of genes coding for an antigen recognized by
autologous cytolytic T lymphocytes on a human melanoma
J. Exp. Med. 182 (3), 689-698 (1995)
JOURNAL
MEDLINE 95378788
PUBMED 7544395
REFERENCE 2 (bases 1 to 527)
AUTHORS Van den Eynde,B.J.
TITLE Direct Submission
JOURNAL Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute
for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium
FEATURES
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BEVKTPEEGKXQSQ"

ORIGIN
Query Match 96.7%; Score 522.2; DB 9; Length 527;
Best Local Similarity 99.4%; Pred. No. 1.2e-124;
Matches 524; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCACGGAGCTGTGAGGACGAGTGTGTGTGTCTTCTGCGTCCGCGACTCTTTTCTCTAC 61
Db 1 GCCAGGAGCTGTGAGGACGAGTGTGTGTGTCTTCTGCGTCCGCGACTCTTTTCTCTAC 60
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QY 62 TGAGATTCACTCTGTGTAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGA 121
Db |||
QY 61 TGAGATTCACTCTGTGTAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGA 120
Db |||
QY 122 CCAAGGCGGTATGTACAGCCTCTCTGAAATGATTGGGCTATGCGGCCCGGAGCAGTTTCAGT 181
Db |||
QY 121 CCAAGGCGGTATGTACAGCCTCTCTGAAATGATTGGGCTATGCGGCCCGGAGCAGTTTCAGT 180
QY 182 GATGAAGTGAACACAGCAACACCTGAGAGGGGAACCAAGCAACTCAAAGTCAGGATCCT 241
Db |||
QY 181 GATGAAGTGAACACAGCAACACCTGAGAGGGGAACCAAGCAACTCAAAGTCAGGATCCT 240
QY 242 GCAGCTGCTCAGGAGGAGAGGATGAGGGAGCATCTGAGGTCAAGGGCCGAGACCTGAA 301
Db |||
QY 241 GCAGCTGCTCAGGAGGAGAGGATGAGGGAGCATCTGAGGTCAAGGGCCGAGACCTGAA 300
QY 302 GCTGATAGCCAGGAAACAGGGTCAACCAAGACTGGGTGTGAGTGTGAAGATGGTCTCTGAT 361
Db |||
QY 301 GCTGATAGCCAGGAAACAGGGTCAACCAAGACTGGGTGTGAGTGTGAAGATGGTCTCTGAT 360
QY 362 GGGCAGGAGATGGACCCGCCAATCCAGAGGAGGTGAAAACGCTGAAAGGTGAAAAG 421
Db |||
QY 361 GGGCAGGAGTGGACCCGCCAATCCAGAGGAGGTGAAAACGCTGAAAGGTGAAAAG 420
QY 422 CAATCACAGTGTAAAAGAAAGCACCGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAT 481
Db |||
QY 421 CAATCACAGTGTAAAAGAAAGCACCGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAT 480
QY 482 TTGTTCAATAAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAA 528
Db |||
QY 481 TTGTTCAATAAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAA 527
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Search completed: August 6, 2004, 17:39:47  
Job time : 2251 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 13:18:49 ; Search time 2416 Seconds

(without alignments)  
6674.494 Million cell updates/sec

Title: US-09-782-745-16

Perfect score: 540

Sequence: 1 CGCCAGGGAGCTGTGGGCA.....CTGCAGAAAAA.....540

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 28726800

Minimum DB seq length: 0

Maximum DB seq length: 540

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Est:\*

1: em estba:\*

2: em esthum:\*

3: em estin:\*

4: em estmu:\*

5: em estov:\*

6: em estpl:\*

7: em estro:\*

8: em htc:\*

9: gb est1:\*

10: gb est2:\*

11: gb htc:\*

12: gb est3:\*

13: gb est4:\*

14: gb est5:\*

15: em estfun:\*

16: em estom:\*

17: em gss\_hum:\*

18: em gss\_inv:\*

19: em gss\_pln:\*

20: em gss\_vrt:\*

21: em gss\_fun:\*

22: em gss\_nam:\*

23: em gss\_mus:\*

24: em gss\_pro:\*

25: em gss\_rod:\*

26: em gss\_phg:\*

27: em gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	530.6	98.3	537	12	BM832793
2	514.2	95.2	527	12	BI826605
3	513.6	95.1	521	13	EX108227
4	508.2	94.1	517	14	CF780547

5	498.2	92.3	509	12	BI868671
6	473.2	87.6	489	9	AA447559
7	455.4	84.3	457	10	AW510753
8	446.8	82.7	464	9	AA738037
9	442.2	81.9	447	9	AI381509
10	438.6	81.2	480	12	BGI20336
11	437.6	81.0	505	14	CB115693
12	431.6	79.9	450	9	AA760996
13	420.2	77.8	455	9	AI187350
14	410.6	76.0	418	9	AW016546
15	402	74.4	426	9	AA868226
16	379.4	70.3	383	12	BM836228
17	379.2	70.2	419	9	AA448542
18	378.6	70.1	445	11	BC005363
19	363.8	67.4	412	9	AW102587
20	340.6	63.1	383	13	BX283580
21	336	62.2	384	9	AA913206
22	318.8	59.0	397	12	BG206349
23	317.4	58.8	341	12	BP431265
24	315.6	58.4	398	9	AA918604
25	310.4	57.5	320	12	BM836021
26	308.8	57.2	333	13	BUS33718
27	276.2	51.1	457	14	CF780497
28	271.4	50.3	275	14	CB147043
29	271.4	50.3	275	14	CB150355
30	271.4	50.3	275	14	CB157288
31	248.8	46.1	256	12	BG181480
32	230.2	42.6	258	12	BG186708
33	225	41.7	253	12	BG184057
34	225	41.7	261	12	BG190600
35	221.6	41.0	245	12	BG212621
36	218.2	40.4	292	12	BG212622
37	214.8	39.8	245	12	BG208433
38	209.2	38.7	507	9	AA972716
39	208	38.5	224	9	AA738394
40	207	38.3	256	12	BG218461
41	206.8	38.3	524	11	AF318372
42	197.2	36.5	520	14	CB961487
43	197	36.5	197	9	AI968311
44	192.8	35.7	226	12	BG220441
45	192.4	35.6	499	12	BG354572

## ALIGNMENTS

RESULT 1	BM832793	537 bp	mRNA	linear	EST 06-MAR-2002
BM832793	K-EST0107334	S5SNU484s1	Homo sapiens	CDNA clone	S5SNU484s1-8-F10
LOCUS	5', mRNA sequence.				
DEFINITION	BM832793				
ACCESSION	BM832793				
VERSION	BM832793.1				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.U., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.				
TITLE	21C Frontier Korean EST Project 2001				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 8 row: F column: 10 High quality sequence stop: 537.				

## FEATURES

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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
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 /cell\_line="Epithelial"  
 /cell\_line="SNU-484"  
 /lab\_host="Top10P"  
 /clone\_lib="S55NU484s1"  
 /note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was decapped with tobacco acid pyrophosphatase (TAP) and ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase. The first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(dR)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10P with electroporation method."

## ORIGIN

Query Match 98.3%; Score 530.6; DB 12; Length 537;  
 Best Local Similarity 99.3%; Pred. No. 1.5e-98;  
 Matches 533; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GCCAGGGAGCTGAGGAGGCTGTGGTCTTCGCGTCCGAGCTCTTTCTCTAC 61  
 DB 1 GCCAGGGAGCTGAGGAGGCTGTGGTCTTCGCGTCCGAGCTCTTTCTCTAC 60

QY 62 TGAGATTTCATCTGTGAAATATGAGTTGGCGAGAGATCGACCTATTATTGGCCTAGA 121  
 DB 61 TGAGATTTCATCTGTGAAATATGAGTTGGCGAGAGATCGACCTATTATTGGCCTAGA 120

QY 122 CCAAGCGCTATGTACGCCCTCTCGAATGATTTGGGCTATGGCGCCGAGCAGTTCA 181  
 DB 121 CCAAGCGCTATGTACGCCCTCTCGAATGATTTGGGCTATGGCGCCGAGCAGTTCA 180

QY 182 GATGAAGTGGACAGACACCTCAAGAGGGAAACAGCAACTCAACGTCAGGATCCT 241  
 DB 181 GATGAAGTGGACAGACACCTCAAGAGGGAAACAGCAACTCAACGTCAGGATCCT 240

QY 242 GCAGCTGTCTCAGGAGGAGAGGATGAGGAGCATCTGCAGGTCAGAGGCCGAGCCTGAA 301  
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QY 302 GCTGATAGCAGGAACAGGTCACCCACAGACTGGTGTGAGTGTGAAGATGCTCTGAT 361  
 DB 301 GCTCATAGCAGGAACAGGTCACCCACAGACTGGTGTGAGTGTGAAGATGCTCTGAT 360

QY 362 GGGCAGGAGATGACCCCGCAATCCAGAGGAGTGAACCGCTCAAGAGAGGTGAAAG 421  
 DB 361 GGGCAGGAGATGACCCCGCAATCCAGAGGAGTGAACCGCTCAAGAGAGGTGAAAG 420

QY 422 CAATCACAGTGTAAAGAGGACGCTTGAATGATGACGGCTGCTCTCTATTTGGAAAT 481

DB 421 CAATCACAGTGTAAAGAGGACACGCTTGAATGATGCGGGTGTCTCTATTTGGAAAT 480

QY 482 TTGTTTCATTAAATCTCCCAATAAAGCTTTACAGCTTTCTGCAAAAAA 538  
 DB 481 TTGTTTCATTAAATCTCCCAATAAAGCTTTACAGCTTTCTGCAAAAAA 537

RESULT 2  
 BI826605 527 bp mRNA linear EST 04-OCT-2001  
 LOCUS 60307056F1 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:516892 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BI826605  
 VERSION BI826605.1 GI:15938155  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 527)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM11419 row: p column: 13  
 High quality sequence stop: 519.  
 Location/Qualifiers  
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 /clone="IMAGE:516892"  
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 /lab\_host="DH10B"  
 /clone\_lib="NIH\_MGC\_119"  
 /note="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH\_MGC Library."

ORIGIN  
 Query Match 95.2%; Score 514.2; DB 12; Length 527;  
 Best Local Similarity 98.5%; Pred. No. 3.3e-95;  
 Matches 519; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 11 CTGTGAGCAGTGTGTGTCTCTCGCGTCCGAGCTCTTTCTCTCTACTGAGATTCA 70  
 DB 1 CTGTGAGCAGTGTGTGTCTCTCGCGTCCGAGCTCTTTCTCTCTACTGAGATTCA 60

QY 71 TCTGTGTGAATATGAGTTGGCGAGGAGATCGACCTATTATTGGCTTAGACCAAGGCG 130  
 DB 61 TCTGTGTGAATATGAGTTGGCGAGGAGATCGACCTATTATTGGCTTAGACCAAGGCG 120

QY 131 TATGTACAGCTCTGAAATGATTGGGCTATGGGCGCCGAGCAGTTCAGTGATCAAGTG 190  
 DB 121 TATGTACAGCTCTGAAATGATTGGGCTATGGGCGCCGAGCAGTTCAGTGATCAAGTG 180

QY 191 GAACCCAGCAACCTGAAAGAGGGGAACAGCAACTCAACGTCAGGATCTCTGAGCTGCT 250  
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Db 241 CAGGAGGAGAGGATCAGGAGGATCTGCAGGTCAGAGGCCGAGGCTGAAGCTCAGC 300
QY 311 CAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGCAGGAG 370
Db 301 CAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGCAGGAG 360
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Db 361 ATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCCTGAAGAGGTTGAAAAGCAATCACAG 420
QY 431 TGTAAAAAGAGCGACGTTGAAATGATGAGGCTGCTCTATCTTGGAAATTTGTCATT 490
Db 421 TGTAAAAAGAGCGACGTTGAAATGATGAGGCTGCTCTATCTTGGAAATTTGTCATT 480
QY 491 AAAATTTCTCCCAATAAAGCTTTACAGCTTCTGCAAAAAA 537
Db 481 AAAATTTCTCCCAATAAAGCTTTACAGCTTCTGCAAAAGAAAAA 527

RESULT 3
BX108227
LOCUS
DEFINITION BX108227 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE998K213161 ;
ACCESSION BX108227
VERSION BX108227.1 GI:27835080
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 521)
AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
HUMAN UNIGENESET - RZPD3
Unpublished (2003)
CONTACT: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE998K213161.
RZPDLIB: I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972);
http://www.rzpd.de/Clonecards/cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACAGGAAACAGCTATGAC.

FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE998K213161 ; IMAGE:1256204"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP GC3"
/notes="Vector: pTV73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pTV73
vector. Library is not normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo. "
```

```
Query Match 95.1%; Score 513.6; DB 13; Length 521;
Best Local Similarity 99.2%; Pred. No. 4.4e-95;
Matches 516; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 19 CAGTGTGTGTGTTCTTCGCGTCCGCGACTCTTTTTCCTCTACTGAGATTCACTCTGTG 78
Db 1 CAGTGTGTGTGTTCTTCGCGTCCGCGACTCTTTTTCCTCTACTGAGATTCACTCTGTG 60
QY 79 AAATATGATTTGGCCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGCGCTATGTACA 138
Db 61 AAATATGATTTGGCCGAGGAAGATCGACCTGTTATTGGCCCTAGTCCAAAGAGCTATGTACA 120
QY 139 GCCTCTGAAATGATTTGGCCCTATGGGCCCCGAGCAGTTTCAGTGTGAAGTGAACCCAGC 198
Db 121 GCCTCTGAAATGATTTGGCCCTATGCAGCCCCGAGCAGTTTCAGTGTGAAGTGAACCCAGC 180
QY 199 AACACCTGAAGAAAGGGGAACCCAGCACTCAACGTGAGGATCTTCGACGCTGCTCAGGAGG 258
Db 181 AACACCTGAGAAAGGGGAACCCAGCACTCAACGTGAGGATCTTCGACGCTGCTCAGGAGG 240
QY 259 AGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAGCCCTGAAGCTGTAGTATGACGAGCA 318
Db 241 AGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAGCCCTGAAGCTGTAGTATGACGAGCA 300
QY 319 GGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGTATGGCAGAGATGAGACCC 378
Db 301 GGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGTATGGCAGAGATGAGACCC 360
QY 379 GCCAATCCAGAGGAGGTGAAAACGCCCTGAAGAGTGAAGCAATCACAGTGTAAAAA 438
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QY 439 GAAGCAGCTTGAAATGATGAGGCTGCTCTATGTGTGAAATTTGTTCAATAATTTCT 498
Db 421 GAAGCAGCTTGAAATGATGAGGCTGCTCTATGTGTGAAATTTGTTCAATAATTTCT 480
QY 499 CCCAATAAGCTTTACAGCCTTCGCAAAAAA 538
Db 481 CCCAATAAGCTTTACAGCCTTCGCAAAAAA 520

RESULT 4
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LOCUS
DEFINITION AGENCOURT_15739102 NIH MGC.217 Homo sapiens cDNA clone
IMAGE:30524555 5', mRNA sequence.
ACCESSION CF780547
VERSION CF780547.1 GI:37739989
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 517)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
CONTACT: Daniela S. Gerhard, Ph.D.
OFFICE OF Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapsb-remail.nih.gov
Tissue Procurement: James Martin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM604 row: e column: 12
High quality sequence stop: 517.
Location/Qualifiers
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/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC 217"
/notes="Vector: pYX-Asc; Site 1: EcoRI; Site 2: NotI;
Library is oligo-dT primed and directionally cloned
Denatured RNA was size fractionated on a 1% agarose gel.
First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated with
EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. Average insert size
0.5-1kb. Adaptors 5' (AATTCGACGAGG) 3' and 5'd
(CCTGCGCGC) 3'. 3' linker sequence - GCGCGCGCTGAGAGCC T18.
Sequencing primers 3' end: T3 promoter primer 5'd
(ATTAACCCCTCACTAAAGGA) 3'. 5' End: T7 promoter primer 5'd
(TAATAGCATCACTAGGG) 3'. Average insert size 0.5-1kb.
Library was constructed in the laboratory of M. Bento
Soares. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 94.1%; Score 508.2; DB 14; Length 517;
Best Local Similarity 99.4%; Pred. No. 5.7e-94;
Matches 510; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 13 GTGAGGAGTGTGTGGTTCCTGCGGTCCGGAGTCTTTTCTCTACTGAGATTCATC 72
Db 4 GAGGGGAGTGTGTGGTTCCTGCGGTCCGGAGTCTTTTCTCTACTGAGATTCATC 63

Qy 73 TGTGTGAATATGATTTGGGAGGAAGATCGACCTATTATTGGCTAGACCAAGCGCTA 132
Db 64 TGTGTGAATATGATTTGGGAGGAAGATCGACCTATTATTGGCTAGACCAAGCGCTA 123

Qy 133 TGTACAGCCTCCTGAAATGATTTGGGCTTATGCGGCCGAGCAGTTTCAGTGAAGTGA 192
Db 124 TGTACAGCCTCCTGAAATGATTTGGGCTTATGCGGCCGAGCAGTTTCAGTGAAGTGA 183

Qy 193 ACAGCAACCTGAGAGGGGAAACAGCAACTCAAGTCAAGCTGAAGTGAAGTGA 252
Db 184 ACCAGCAACCTGAGAGGGGAAACAGCAACTCAAGTCAAGTGAAGTGAAGTGA 243

Qy 253 GGAGGAGAGGATCAGGAGCATCTGCAGGTCAAGGCGGAGGCTGAAGTGAAGTGA 312
Db 244 GGAGGAGAGGATCAGGAGCATCTGCAGGTCAAGGCGGAGGCTGAAGTGAAGTGA 303

Qy 313 GGAAACAGGCTCACCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGCAGGAGAT 372
Db 304 GGAACAGGCTCACCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGCAGGAGAT 363

Qy 373 GGACCCGCAATCAGAGGAGGTGAACCCCTGAAGAGGTGAAGAGCATCAGAGT 432
Db 364 GGACCCGCAATCAGAGGAGGTGAACCCCTGAAGAGGTGAAGAGCATCAGAGT 423

Qy 433 TTAAGAAGGACGTTGAATGATGAGGCTGCTCTATCTTGGAAATTTGTTCAATTA 492
Db 424 TTAAGAAGGACGTTGAATGATGAGGCTGCTCTATCTTGGAAATTTGTTCAATTA 483

Qy 493 AATTCTCCCAATAAAGCTTTACAGCCTTCTGCA 525
Db 484 AATTCTCCCAATAAAGCTTTACAGCCTTCTGCA 516

RESULT 5
BI868671
LOCUS 603392594F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5402663 5',
DEFINITION mRNA sequence.
ACCESSION BI868671
VERSION BI868671.1 GI:16042344
```

```
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 509)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12026 row: 1 column: 24
High quality sequence stop: 509.
FEATURES
source
1..509
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5402663"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_90"
/notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 92.3%; Score 498.2; DB 12; Length 509;
Best Local Similarity 99.4%; Pred. No. 6.3e-92;
Matches 500; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGCAGGGAGCTGTGAGGAGTGTGTGGTTCCTGCGGTCCGGAGTCTTTTCTCTCTA 60
Db 7 CGCTAGGGAGCTGTGAGGAGTGTGTGGTTCCTGCGGTCCGGAGTCTTTTCTCTCTA 66

Qy 61 CTGAGATTCTCTGTGAAATATGAGTTCGCGAGGAAGATCGACCTATTATTGGCCTAG 120
Db 67 CTGAGATTCTCTGTGAAATATGAGTTCGCGAGGAAGATCGACCTATTATTGGCCTAG 126

Qy 121 ACCAAGCGCTATGTACAGCTCTCTGAAATGATTTGGGCTTATGCGGCCGAGAGTTCAG 180
Db 127 ACCAAGCGCTATGTACAGCTCTCTGAAATGATTTGGGCTTATGCGGCCGAGAGTTCAG 186

Qy 181 TGATGAGTGGACCAACAGTGAAGAGGGGACCAAGTCAAGTCAAGGATCC 240
Db 187 TGATGAGTGGACCAACAGTGAAGAGGGGACCAAGTCAAGTCAAGGATCC 246

Qy 241 TGCAGCTGCTCAGAGGAGGAGTGAAGGAGCATCTGCAGGTCAAGGGCCGAGAGCTGA 300
Db 247 TGCAGCTGCTCAGAGGAGGAGTGAAGGAGCATCTGCAGGTCAAGGGCCGAGAGCTGA 306

Qy 301 AGCTGATAGCAGAAACAGGGTCAACCAAGCTGGGTGTGAGTGAAGTGTCTCTGA 360
Db 307 AGCTGATAGCAGAAACAGGGTCAACCAAGCTGGGTGTGAGTGAAGTGTCTCTGA 366

Qy 361 TGGCAGGAGATGACCCGCCAAATCCAGAGGAGGTGAAAACGCTCAAGAGGTGAAAA 420
Db 367 TGGCAGGAGATGACCCGCCAAATCCAGAGGAGGTGAAAACGCTCAAGAGGTGAAAA 426

Qy 421 GCAATCAAGTGTAAAGAGGACGACCTTGAATGATGAGGAGTGTCTCTATGTTGAAA 480
Db 427 GCAATCAAGTGTAAAGAGGACGACCTTGAATGATGAGGAGTGTCTCTATGTTGAAA 486

Qy 481 TTTGTTCAATAAATTTCTCCAA 503
```



```

Db      487  TTTGTCATTAATAATCTCCAA 509
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AA447559      489 bp      mRNA      linear      EST 04-JUN-1997
zw81ell.sl Soares testis NHT Homo sapiens cDNA clone IMAGE:782636
3', similar to TR:G914905 G914905 GAGE-4 PROTEIN. [1] ;, mRNA
sequence.
AA447559      1 GI:2161229
EST.
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 489)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m3 fwd. ET from Amersham
High quality sequence stop: 427.
Location/Qualifiers
1..489
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:782636"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis NHT"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5]
TGTTACCAATCTGAAGTGGAGCGCGGCCCAATTTTTTTTTTTT 3'}.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaudo."

ORIGIN
Query Match      87.6%; Score 473.2; DB 9; Length 489;
Best Local Similarity 99.2%; Pred. No. 8.4e-87;
Matches 486; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 42  CCGGACTCTTTTCTCTACTGAGATTTCATCTGTGTGAATATGAGTTGGCGAGGAAGAT 101
|||||
Db 489  CCGGACTCTTTTCTCTACTGAGATTTCATCTGTGTGAATATGAGTTGGCGAGGAAGAT 430
|||||
QY 102  CGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCCTCTCGTAATGATTGGCGCTTA 161
|||||
Db 429  CGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCCTCTCGTAATGATT-GGCCTA 371
|||||
QY 162  TCGGGCCCGAGGACTTCAGTGTAGTGAACACGACCACTGAGAGGGGACCGAG 221
|||||
Db 370  TCGGGCCCGAGGACTTCAGTGTAGTGAACACGACCACTGAGAGGGGACCGAG 311
|||||
QY 222  CAACTCAACGTTCAGGATCTGTCAGCTGCTCAGGAGGAGGAGGATGAGGAGCATCTGCAG 281
|||||

Db      310  CAACTCAACGTTCAGGATCTGTCAGCTGCTCAGGAGGAGGAGGATGAGGAGCATCTGCAG 251
|||||
QY 282  GTCAAGGGCCGGAAGCTGAAGCTGATAGCCAGGAACAGGGTTCACCCACAGACTGGGTGTG 341
|||||
Db 250  GTCAAGGGCCGGAAGCTGAAGCTGATAGCCAGGAACAGGGTTCACCCACAGACTGGGTGTG 191
|||||
QY 342  AGTGTGAAGATGCTCTGATGGCGAGGATGGACCCGCCAAATCCAGAGGAGGTGAAA 401
|||||
Db 190  AGTGTGAAGATGCTCTGATGGCGAGGATGGACCCGCCAAATCCAGAGGAGGTGAAA 131
|||||
QY 402  CGCCTGAAGAAGCTGAAAAGCAATCACAGCTTTAAAGAGGACAGCTTCAAAATGATGCAG 461
|||||
Db 130  CGCCTGAAGAAGCTGAAAAGCAATCACAGCTTTAAAGAGGACAGCTTCAAAATGATGCAG 71
|||||
QY 462  GCTGCTCCTTANGTGGAAATTTGTTCAATTAATTTCTCCCAATAAAGCTTTTACAGCTTC 521
|||||
Db 70  GCTGCTCCTTANGTGGAAATTTGTTCAATTAATTTCTCCCAATAAAGCTTTTACAGCTTC 11
|||||
QY 522  TCCAAAAAA 531
|||||
Db 10  TCCAAAAAA 1
|||||

RESULT 7
AW510753      457 bp      mRNA      linear      EST 03-MAR-2000
hd39d05.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2911881 3' similar to SW:GGB4_HUMAN Q13068 GAGE-4 PROTEIN. ;,
mRNA sequence.
AW510753      1 GI:7148831
EST.
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 457)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
Location/Qualifiers
1..457
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2911881"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaudo."

ORIGIN
Query Match      84.3%; Score 455.4; DB 10; Length 457;
Best Local Similarity 99.8%; Pred. No. 3.7e-83;
Matches 456; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 76 GTCAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGGCGCTATGT 135  
 Db 457 GTGAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGGCGCTATGT 398  
 QY 136 ACAGCCTCTGAATGATGAGGCTATGCGGCCGAGCAGTTCAGTGAATGAAAGTGAACC 195  
 Db 397 ACAGCCTCTCTGAATGATGAGGCTATGCGGCCGAGCAGTTCAGTGAATGAAAGTGAACC 338  
 QY 196 AGCAACACCTTGAAGAGGGGACACGCAACTCAGCTCAGGATCCTGCAGCTCTCAGGA 255  
 Db 337 AGCAACACCTTGAAGAGGGGACACGCAACTCAGCTCAGGATCCTGCAGCTCTCAGGA 278  
 QY 256 GCGAGAGGATGAGGAGCAGTCTGAGGCTCAAGGCCGAGCCTGAAGCTCATAGCCACGA 315  
 Db 277 GCGAGAGGATGAGGAGCAGTCTGAGCTCAAGGCCGAGCCTGAAGCTCATAGCCACGA 218  
 QY 316 ACAGGGTCAACCCAGACACTGGGTGTGAGTGTGAAGATGGTCTGATGGGAGGAGATGGA 375  
 Db 217 ACAGGGTCAACCCAGACACTGGGTGTGAGTGTGAAGATGGTCTGATGGGAGGAGATGGA 158  
 QY 376 CCGGCCAAATCCAGAGGAGTGAACCGCTGAGAGAGGTGAAGCAATCACAGTGTGA 435  
 Db 157 CCGGCCAAATCCAGAGGAGTGAACCGCTGAGAGAGGTGAAGCAATCACAGTGTGA 98  
 QY 436 AAAGAAGGCGAGTTGAATGATGAGGCTGCTCCTATGTTGGAAATTTGTTCAATAAAT 495  
 Db 97 AAAGAAGGCGAGTTGAATGATGAGGCTGCTCCTATGTTGGAAATTTGTTCAATAAAT 38  
 QY 496 TCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAAA 532  
 Db 37 TCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAAA 1

RESULT 8  
 AA738037/c  
 LOCUS  
 DEFINITION  
 nxl5ell.s1 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1256204 3',  
 similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;, mRNA sequence.  
 AA738037  
 AA738037.1 GI:2768794  
 EST.  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 464)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
 Insert Length: 511 Std Error: 0.00  
 Seq primer: -40ml3 fwd. ET from Amersham  
 High quality sequence stop: 435.  
 Location/Qualifiers  
 1. 464  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1256204"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI-CGAP GC3"  
 /note="vector: pT7T3D-Pac (Pharmacia) with a modified source

polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 82.7%; Score 446.8; DB 9; Length 464;  
 Best Local Similarity 98.8%; Pred. No. 2.1e-81;  
 Matches 451; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 83 ATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGGCGCTATGTACAGCCT 142  
 Db 464 ATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTAGTCCAGACGCTATGTACAGCCT 405  
 QY 143 CCTGAAATGATGGGCTATGCGGCCGAGCAGTTCAGTGAATGAAAGTGAACCAAGCAACA 202  
 Db 404 CCTGAAATGATGGGCTATGCGGCCGAGCAGTTCAGTGAATGAAAGTGAACCAAGCAACA 345  
 QY 203 CCTGAAAGAGGGGAACCCAGCAACTCAGCTCAGGATCCTCAGCTGCTCAGGAGGAGAG 262  
 Db 344 CCTGAAAGAGGGGAACCCAGCAACTCAGCTCAGGATCCTCAGCTGCTCAGGAGGAGAG 285  
 QY 263 GATGAGGAGCATCTGCGAGTCAAGGCCGAGGCTGAAGCTGATGCCAGGAACAGGGT 322  
 Db 284 GATGAGGAGCATCTGCGAGTCAAGGCCGAGGCTGAAGCTGATGCCAGGAACAGGGT 225  
 QY 323 CACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGGAGGAGATGGACCCGCCA 382  
 Db 224 CACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGGAGGAGATGGACCCGCCA 165  
 QY 383 AATCCAGAGGAGTGAACCGCTGAGAGAGGTGAAGCAATCACAGTGTATAAAGAAG 442  
 Db 164 AATCCAGAGGAGTGAACCGCTGAGAGAGGTGAAGCAATCACAGTGTATAAAGAAG 105  
 QY 443 GCACGTTGAATGATGCGAGGCTGCTCCTATGTTGGAAATTTGTTCAATAAATTTCTCCCA 502  
 Db 104 GCACGTTGAATGATGCGAGGCTGCTCCTATGTTGGAAATTTGTTCAATAAATTTCTCCCA 45  
 QY 503 ATAAAGCTTACAGCCTTCTGCAAAAAA 540  
 Db 44 ATAAGAGTTTACAGCCTTCTGCAAAAAA 7

RESULT 9  
 AI381509/c  
 LOCUS  
 DEFINITION  
 te76b07.x1 Soares NFL T.GBC S1 Homo sapiens cDNA clone  
 IMAGE:2092597 3', similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;,  
 mRNA sequence.  
 AI381509  
 AI381509.1 GI:4194290  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 447)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 Insert Length: 497 Std Error: 0.00  
 Seq primer: -40UP from Gibco.  
 Location/Qualifiers  
 1. 447  
 /organism="Homo sapiens" source

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/mol_type="mrna"  
/db_xref="taxon:9606"  
/clone="IMAGE:2092597"  
/lab_host="DH10B"
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/clone_lib="Soares_NFL_T_GBC_S1"  
/notes="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with  
a modified polylinker; Site 1: Not I; Site 2: Eco RI;  
Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung NBHL19W, testis NHT, and B-cell  
NCL CGAP_GCB1) were mixed, and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made  
from the same 3 libraries. The pools consisted of  
I.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento  
Soares and M. Fatima Bonaldo."
```

## ORIGIN

```
Query Match 81.9%; Score 442.2; DB 9; Length 447;  
Best Local Similarity 99.3%; Pred. No. 1.9e-80;  
Matches 444; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 87 GTTGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGGCGCTATGTACAGCCTCTG 146  
Db |||  
447 GTTGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGGCGCTATGTACAGCCTCTG 388  
QY 147 AATGATNTGGGCTATCGGCGCGGAGCAGTTCAGTGATGAATGGAAACAGCAACACCTG 206  
Db |||  
387 AATGATNTGGGCTATCGGCGCGGAGCAGTTCAGTGATGAATGGAAACAGCAACACCTG 328  
QY 207 AAGAGGGGAAACAGCAACTCAACGTCAGGATCTCGAGTCTGCTCAGGAGGAGGAGTG 266  
Db |||  
327 AAGAGGGGAAACAGCAACTCAACGTCAGGATCTCGAGTCTGCTCAGGAGGAGGAGTG 268  
QY 267 AGGAGCATCTCGAGTCAAGGCGCGGAGCCCTGAAGCTGATAGCCAGGAAACAGGCTCACC 326  
Db |||  
267 AGGAGCATCTCGAGTCAAGGCGCGGAGCCCTGAAGCTGATAGCCAGGAAACAGGCTCACC 208  
QY 327 CACAGACTGGGTGTCAGTGTGAAGTGTCTCTGATGGGCGAGAGATGGACCCGCAATC 386  
Db |||  
207 CACAGACTGGGTGTCAGTGTGAAGTGTCTCTGATGGGCGAGAGATGGACCCGCAATC 148  
QY 387 CAGAGGAGTGAAGACCGCTGAAGAGGTGAAAAGCAATCACAGTGTGTTAAAAGAGGAC 446  
Db |||  
147 CAGAGGAGTGAAGACCGCTGAAGAGGTGAAAAGCAATCACAGTGTGTTAAAAGAGACAC 88  
QY 447 GTTGAATGATCGAGCTGCTCTATGTTGGAAATTTGTTTCAATTAATAATCTCCCAATAA 506  
Db |||  
87 GTTGAATGATCGAGCTGCTCTATGTTGGAAATTTGTTTCAATTAATAATCTCCCAATAA 28  
QY 507 AGCTTTACAGCCTTCTGCAAAAAAAA 533  
Db |||  
27 AGCTTTACAGCCTTCTGCAAAAAAAA 1
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RESULT 10  
BG120336

LOCUS BG120336 480 bp mRNA linear EST 30-JAN-2001  
DEFINITION 602353732F1 NTH\_MGC\_90 Homo sapiens cDNA clone IMAGE:4451958 5',  
mRNA sequence.

ACCESSION BG120336

VERSION BG120336.1 GI:12613845

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 480)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.lnl.gov>

Plate: LLAM10239 row: p column: 07

High quality sequence stop: 480.

## FEATURES

source

1..480

/organism="Homo sapiens"

/mol\_type="mrna"

/db\_xref="taxon:9606"

/clone="IMAGE:4451958"

/tissue\_type="adenocarcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NTH\_MGC\_90"

/note="Organ: liver; Vector: pCMV-Sport6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally; oligo-dT primed.

Average insert size 1.7 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NTH\_MGC Library."

## ORIGIN

```
Query Match 81.2%; Score 438.6; DB 12; Length 480;  
Best Local Similarity 99.1%; Pred. No. 1e-79;  
Matches 441; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 96 GAAGATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCCTCTGAAATGATTG 155  
Db |||  
1 GAAGATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCCTCTGAAATGATTG 60  
QY 156 GGCCTATGCGGCCGAGCAGTTCAGTGTGAAGTGGAAACAGCAACACCTGAAGAAGGGG 215  
Db |||  
61 GGCCTATGCGGCCGAGCAGTTCAGTGTGAAGTGGAAACAGCAACACCTGAAGAAGGGG 120  
QY 216 AACAGCAACTCAACGTCAGGATCTCGAGTGTCTCAGAGGGGAGGAGTGAAGGAGCAT 275  
Db |||  
121 AACAGCAACTCAACGTCAGGATCTCGAGTGTCTCAGAGGGGAGGAGTGAAGGAGCAT 180  
QY 276 CTGCAAGGTCAGGGCCGAGCCTGAGCTGTAGCCAGGAAACAGGTCACCCACAGACTG 335  
Db |||  
181 CTGCAAGGTCAGGGCCGAGCCTGAGCTGTAGCCAGGAAACAGGTCACCCACAGACTG 240  
QY 336 GGTGTGAGTGTGAAGATGGTCTCTGATGGCGAGGATGGACCCGCAANTCCAGAGGAGG 395  
Db |||  
241 GGTGTGAGTGTGAAGATGGTCTCTGATGGCGAGGATGGACCCGCAANTCCAGAGGAGG 300  
QY 396 TGAACAACGCTGAAGAAGGTGAAAAAGCAATCACAGTGTGTTAAAGAGGACGCTTGAAATG 455  
Db |||  
301 TGAACAACGCTGAAGAAGGTGAAAAAGCAATCACAGTGTGTTAAAGAGGACGCTTGAAATG 360  
QY 456 ATGCAAGGTCGCTCTCTATGTTGGAATTTGTTTCAATTAATAATCTCCCAATAAGCTTTTACA 515  
Db |||  
361 ATGCAAGGTCGCTCTCTATGTTGGAATTTGTTTCAATTAATAATCTCCCAATAAGCTTTTACA 420  
QY 516 GCCTTCTGCAAAAAAAA 540  
Db |||  
421 GCCTTCTGCAAAAAAAA 445
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RESULT 11

CB115693

LOCUS

DEFINITION

sequence.

ACCESSION

CB115693

VERSION

CB115693.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

CB115693

K-EST0159805 L8SCK0 Homo sapiens cDNA clone L8SCK0-8-B09 5', mRNA

sequence.

ACCESSION

CB115693

VERSION

CB115693.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 505)  
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
Kim,Y.S.  
21C Frontier Korean EST Project 2001  
Unpublished (2002)  
Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel.: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.krribb.re.kr  
Plate: 8 row: B column: 09  
High quality sequence stop: 505.  
Location/Qualifiers

source  
1. .505  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="L8SCK0-8-B09"  
/sex="M"  
/cell\_line="SCK"  
/lab\_host="Top10p"  
/clone\_lib="L8SCK0"  
/note="Organ: Liver; Vector: pT73-Pac; Site 1: EcoRI;  
Site 2: NotI; The library was contributed by the Soares  
laboratory and it was constructed as described by Bonaldo,  
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research  
6(9): 791-806. RNA was prepared from harvested cell  
culture."

## FEATURES

source

## ORIGIN

Query Match 81.0%; Score 437.6; DB 14; Length 505;  
Best Local Similarity 98.0%; Pred. No. 1.6e-79;  
Matches 443; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
Qy 31 GTTCTCGGTCGGACTCTTTTCCCTACTGAGTTCATCTGTGGAATAGATTG 90  
Db 19 GGTCTCGGTCGGACTCTTTTCCCTACTGAGTTCATCTGTGGAATAGATTG 78  
Qy 91 GCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGCGCTATCTACAGCCTCTCTGAAAT 150  
Db 79 GCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGCGCTATCTACAGCCTCTCTGAAAT 138  
Qy 151 GATTGGCCCTATGCGGCCGAGCAGTTCAGTGATGAAGTGAAACAGCAACCTTGAGA 210  
Db 139 GATTGGCCCTATGCGGCCGAGCAGTTCAGTGATGAAGTGAAACAGCAACCTTGAGA 198  
Qy 211 AGGGGAACCACTCAACCTCAGGATCCTGCGAGCTCTCAGGAGGAGGATGAGGG 270  
Db 199 AGGGGAACCACTCAACCTCAGGATCCTGCGAGCTCTCAGGAGGAGGATGAGGG 258  
Qy 271 AGCATCTCGAGTCAAGGGCCGAGCCTGAAGCTGATAGCCAGAAACAGGCTCACCCACA 330  
Db 259 AGCATCTCGAGTCAAGGGCCGAGCCTGAAGCTGATAGCCAGAAACAGGCTCACCCACA 318  
Qy 331 GACTGGGTGTGAGTGTGAAGATGGTCTGTGATGGGAGGAGATGGAACCCGCAATCCAGA 390  
Db 319 GACTGGGTGTGAGTGTGAAGATGGTCTGTGATGGGAGGAGATGGAACCCGCAATCCAGA 378  
Qy 391 GGAGGTGAACCGCTGAAGAGGTGAACCAATCAAGTGTAAAGAGGAGGACGCTTG 450  
Db 379 GGAGGTGAACCGCTGAAGAGGTGAACCAATCAAGTGTAAAGAGGAGGACGCTTG 438  
Qy 451 AAATGATCAGGCTGCTCTCTATGTTGGAAAT 482  
Db 439 AAATGATCAGGCTGCTCTCTATGTTGGAAAT 470

RESULT 12

AA760996/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA760996 450 bp mRNA linear EST 26-JAN-1998  
tx32h08.s1 NCI-CGAP GC4 Homo sapiens cDNA clone IMAGE:1257855 3',  
similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ; mRNA sequence.  
AA760996  
AA760996.1 GI:2809926  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 450)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Seq primer: -40m13 fwd. RT from Amersham  
High quality sequence stop: 331.  
Location/Qualifiers

source

FEATURES

1. .450

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1257855"

/tissue\_type="pooled germ cell tumors"

/lab\_host="DH10B"

/clone\_lib="NCI-CGAP GC4"

/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from 3 pooled  
germ cell tumors, and was then primed with a Not I -  
oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified pT73  
vector. Library is normalized. Library was constructed by  
Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 79.9%; Score 431.6; DB 9; Length 450;  
Best Local Similarity 98.7%; Pred. No. 2.8e-78;  
Matches 445; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
Qy 83 ATGAGTTGGCAGGAAGATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCT 142  
Db 450 ATGAGTTGGCAGGAAGATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCT 391  
Qy 143 CCTGAAATGATGGGCCCTATCGGCCCGCAGCAGTTCAGTGATGAAGTGAACACGACA 202  
Db 390 CCTGAAGTGAAGTGGTCTATCGGCCCGCAGCAGTTCAGTGATGAAGTGAACACGACA 331  
Qy 203 CCTGAAAGGGGAGCAACGACNACTCAAGCTCAGGATCCTGCGCTGCTCAGGAGGAGAG 262  
Db 330 CCTGAAAGGGGAGCAACGACNACTCAAGCTCAGGATCCTGCGCTGCTCAGGAGGAGAG 271  
Qy 263 GATCAGGAGCATCTGCAAGGTCAGAGGCCAGGCTCAAGCTGATAGCTAGCCAGGAACAGGGT 322  
Db 270 GATCAGGAGCATCTGCAAGGTCAGAGGCCAGGCTCAAGCTGATAGCTAGCCAGGAACAGGGT 211  
Qy 323 CACCCACAGACTGGTGTGAGTGTGAAGTGGTCTCTGATGGCAGGAGATGGAACCCGCA 382  
Db 210 CACCCACAGACTGGTGTGAGTGTGAAGTGGTCTCTGATGGCAGGAGATGGAACCCGCA 151  
Qy 383 AATCCAGAGGAGTGAAGCCCTGAAGAGTGAAGAGCAATCACAGTGTAAAGAGAG 442



NCI CGAP Lu19, NCI CGAP GC4, NCI CGAP GC6, NCI CGAP Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below: NCI CGAP Kid3 pool 1 LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE.CloneIDs 1322376-1323911, 1456008-1456775, 1500552-1502855) NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE.CloneIDs 1323912-1325831, 1471368-1472903, 1492104-1493255) NCI CGAP Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE.CloneIDs 1414920-1417991, 1520904-1522439) NCI CGAP GC4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE.CloneIDs 1257096-1258631, 1469064-1470983, 1475592-1476743) NCI CGAP Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE.CloneIDs 985608-986759, 1101192-1101959, 1217928-1220615) NCI CGAP Col0 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE.CloneIDs 1057416-1061255, 1144584-1145351) The resulting ClonEDs 1057416-1061255, 1144584-1145351) The resulting subtracted library contained 4 million recombinants. Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches to Facilitate Gene Discovery. Genome Research 6, 791-806. TAG\_TISSUE=germ cell TAG\_LIB=NCI CGAP\_GC4 TAG\_SEQ=AAATC

## ORIGIN

Query Match 76.0%; Score 410.6; DB 9; Length 418;  
Best Local Similarity 99.0%; Pred. No. 5.6e-74;  
Matches 413; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 124 AAGCGCTATGTACAGCTCTCTGAAATGATTTGGGCTATGGCCGCGAGTTCAGTGA 183  
DB 418 AAGACGCTACGTAGAGCTCTCTGAAATGATTTGGGCTATGGCCGCGAGTTCAGTGA 359

QY 184 TGAAGTGAACAGCAGCAACACCTGAAGAGCGGACCAAGCACTCAACTCAGAGTCTCTGC 243  
DB 358 TGAAGTGAACAGCAGCAACACCTGAAGAGCGGACCAAGCACTCAACTCAGAGTCTCTGC 299

QY 244 AGCTGCTCAGAGGAGGAGATGAGGGAGCATCTGTGAGGTCAAGGCGCGAAGCTGAAGC 303  
DB 298 AGCTGCTCAGAGGAGGAGATGAGGGAGCATCTGTGAGGTCAAGGCGCGAAGCTGAAGC 239

QY 304 TGATAGCCAGCAACAGGCTCACCCACAGCTGGGTGTGAGTGTGAAGTGTCTCTGATGG 363  
DB 238 TCATAGCCAGCAACAGGCTCACCCACAGCTGGGTGTGAGTGTGAAGTGTCTCTGATGG 179

QY 364 GCAGGAGATGGACCCGCAAAATCCACAGAGAGGTGAAAACGGCTGAAGAGGCTGAAGCA 423  
DB 178 GCAGGAGATGGACCCGCAAAATCCACAGAGAGGTGAAAACGGCTGAAGAGGCTGAAGCA 119

QY 424 ATCAGAGTGTAAAGAGAGCAGTGTGAATGATGAGGCTGTCTCTATGTTGGAATTT 483  
DB 118 ATCAGAGTGTAAAGAGAGCAGTGTGAATGATGAGGCTGTCTCTATGTTGGAATTT 59

QY 484 GTTCATTTAAATCTCCCAATAAGCTTTACAGCTCTCTGCAAAAAAATAAAAAA 540  
DB 58 GTTCATTTAAATCTCCCAATAAGCTTTACAGCTCTCTGCAAAAAAATAAAAAA 2

RESULT 15  
AA868226/c  
LOCUS  
DEFINITION  
ak49h07.s1 Soares testis Nht Homo sapiens cdna clone IMAGE:1409245  
3', similar to SW:GGE2\_HUMAN Q13066 GAGE-2 PROTEIN. [1] ;, mRNA  
sequence.  
ACCESSION  
AA868226.1 GI:2963671  
VERSION  
AA868226  
KEYWORDS  
EST.  
Homo sapiens (human)  
SOURCE  
Homo sapiens  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 426)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-femail.nih.gov](mailto:cgaps-femail.nih.gov)  
cdna Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
cdna Library Arrayed by: Greg Lennon, Ph.D.  
DNA sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Possible reversed clone: similarity on wrong strand  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 363.

FEATURES  
source

1..426  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1409245"  
/sex="male"  
/lab\_host="DH10B"  
/clone\_lib="Soares testis NHT"  
/note="Vector: pT7T3D-Pac-(Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cdna  
was prepared from mRNA obtained from Clontech  
Laboratories, Inc., and primed with a Not I - oligo(dT)  
primer [5].  
TGTTACCAATCTGAAGTGGAGGGCGCGCCCAATTTTTTTTTTTT 3'.  
Double-stranded cdna was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT7T3 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 74.4%; Score 402; DB 9; Length 426;  
Best Local Similarity 97.1%; Pred. No. 3.2e-72;  
Matches 408; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 110 TATTGGCTACACCAAGCGCTATGTACAGCTCTCTGAAATGATTTGGGCTATGCGGCC 169  
DB 420 TATCGGCTAGACCAAGCGCTCTAGAGCTCTCTGAAATGNANTTGCCTATGCGGCC 361

QY 170 GAGCAGTTCAGTGTAGTGAACCCAGCAACACCTGAAGAGGGGAACCAAGCACTCAA 229  
DB 360 GAGCAGTTCAGTGTAGTGAACCCAGCAACACCTGAAGAGGGGAACCAAGCACTCAA 301

QY 230 CGTCAGATCTCGAGCTGCTCAGGAGGAGAGTGAAGGAGCATCTGAGGTCAAGGG 289  
DB 300 CGTCAGATCTCGAGCTGCTCAGGAGGAGAGTGAAGGAGCATCTGAGGTCAAGGG 241

QY 290 CCGAAGCTCTGAAGCTGTAGCCAGCAAGGCTCACCCACAGACTGGGTGTGAGTGTGAA 349  
DB 240 CCGAAGCTCTGAAGCTGTAGCCAGCAAGGCTCACCCACAGACTGGGTGTGAGTGTGAA 181

QY 350 GATGCTCTGTATGGCAGGAGATGACCCGCGCAATCCAGAGGAGTGAACACGCTGAA 409  
DB 180 GATGCTCTGTATGGCAGGAGATGACCCGCGCAATCCAGAGGAGTGAACACGCTGAA 121

QY 410 GAAGGTGAAGAGCATCAGCTGTAAAGAGGAGCAGCTTGAAATGATGCGGCTGCTCC 469  
DB 120 GAAGGTGAAGAGCATCAGCTGTAAAGAGGAGCAGCTTGAAATGATGCGGCTGCTCC 61

QY 470 TATGTTGAAATTTGTTTCATTAATAATCTCCCAATAAGCTTTACAGCTTCTGCAAAA 529  
DB 60 TATGTTGAAATTTGTTTCATTAATAATCTCCCAATAAGCTTTACAGCTTCTTCAAAA 1

Search completed: August 6, 2004, 18:20:17  
Job time : 2420 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 13:00:38 ; Search time 329 Seconds  
(without alignments)  
6972.726 Million cell updates/sec

Title: US-09-782-745-16

Perfect score: 540

Sequence: 1 CGCCAGGAGCTGTGAGGCA.....CTGCAAAAAAAAAAAAAAAAAA 540

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 5025714

Minimum DB seq length: 0

Maximum DB seq length: 540

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002s:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	540	100.0	540	2	AAX90521 GAGE-4 tu
2	534.2	98.9	540	2	AAX90523 GAGE-6 tu
3	528.8	97.9	532	2	AAX90522 GAGE-5 tu
4	528	97.8	528	6	ABL66323 Lung canc
5	524.6	97.1	539	2	AAX18721 cDNA enco
6	522.2	96.7	527	7	ACC51027 Human bla
7	522.2	96.7	527	7	ABL76236 Lung canc
8	520.8	96.4	532	2	AAX18720 cDNA enco
9	512.8	95.0	538	2	AAX90519 GAGE-2 tu
10	508.8	94.2	526	7	ADAI5802 Human GAG
11	504.8	93.5	530	7	ADAI5803 GAGE-2 fu
12	504.4	93.4	528	7	ADAI5801 Human GAG
13	471	87.2	535	2	AAX18717 cDNA enco
14	360.4	66.7	430	3	ACC02129 Human sec
15	306.2	56.7	530	4	AAS60104 Human can
16	304	56.3	365	4	AAS60496 Human can
17	245	45.4	257	7	ABZ19955 Group III
18	245	45.4	264	7	ABZ19755 Group III
19	243.4	45.1	277	7	ABZ19551 Group III
20	229	42.4	229	7	ABZ20497 TP51 subt
21	225.4	41.7	227	7	ABZ20480 TP51 subt
22	224.4	41.6	229	7	ABZ18686 Group III
23	221	40.9	259	7	ABZ19791 Group III

24	210	38.9	520	7	ABT15737 Human can
25	205.6	38.1	225	7	ABZ19533 Group III
26	202.4	37.5	509	7	ABX77605 Different
27	202.4	37.5	509	8	ACD42232 Human GAG
28	202.4	37.5	509	9	ADC24646 Human cdn
29	187	34.6	532	4	AAI60530 Human pol
30	180.6	33.4	219	7	ABZ19538 Group III
31	164.2	30.4	503	5	AAS69484 DNA enco
32	141.6	26.2	528	7	ABT15728 Human can
33	131.6	24.4	475	4	AAD14981 Human can
34	126.6	23.4	538	7	ABT15736 Human can
35	109.6	20.3	399	5	AAF68151 Human can
36	109.6	20.3	399	6	ABK38062 cDNA enco
37	109.6	20.3	399	7	ACA10391 Human lun
38	109.6	20.3	399	7	ABX99342 Lung canc
39	109.6	20.3	399	10	ADF72125 Human lun
40	105.2	19.5	505	6	AAD24228 Human dif
41	105	19.4	463	6	ABA92217 Melanoma
42	103.2	19.1	515	4	AAS63900 Human pro
43	103.2	19.1	515	4	AAS63900 Human pro
44	103.2	19.1	515	4	AAH02872 Prostate
45	103.2	19.1	515	4	AAH85121 Human pro

## ALIGNMENTS

RESULT 1  
AAX90521  
ID AAX90521 standard; cDNA; 540 BP.  
XX  
AC AAX90521;  
XX  
DT 30-SEP-1999 (first entry)  
XX  
DE GAGE-4 tumour rejection antigen clone nucleotide sequence.  
XX  
KW Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection;  
KW therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;  
KW GAGE; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9937665-Al.  
XX  
PD 29-JUL-1999.  
XX  
PF 12-JAN-1999; 99WO-US000775.  
XX  
PR 23-JAN-1998; 98US-00012818.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
XX  
PI Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Falleur T;  
XX  
DR WPI; 1999-469111/39.  
XX  
PT New isolated peptides which bind to HLA-A29 molecules, which are tumor  
PT rejection antigens used for detection and therapy of pathological  
XX conditions, e.g. cancer.  
XX  
PS Example 13; Fig 4; 62pp; English.  
XX  
CC The present invention describes peptides which bind to human leukocyte  
CC antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into  
CC tumour rejection antigens. They can be used for detecting cytolytic T  
CC lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-  
CC typing assays. Complexes of HLA-29 molecules and the peptides can be used  
CC for stimulating CTLs in vivo. The present sequence represents a GAGE  
CC tumour rejection antigen clone, from an example from the present  
XX invention  
SQ Sequence 540 BP; 159 A; 114 C; 156 G; 111 T; 0 U; 0 Other;

PT	rejection antigens used for detection and therapy of pathological conditions, e.g. cancer.
PT	
XX	Example 13; Fig 4; 62pp; English.
PS	
XX	The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic T lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present invention
XX	
SQ	Sequence 540 BP; 159 A; 113 C; 157 G; 111 T; 0 U; 0 Other;
CC	Query Match 98.9%; Score 534.2; DB 2; Length 540;
CC	Best Local Similarity 99.4%; Pred. No. 7.7e-143; Indels 0; Gaps 0;
CC	Matches 536; Conservative 0; Mismatches 3;
QY	2 GCACGGGAGCTGTGAGGACGTGTGTGTGTCTCGCTCGGACCTCTTTTCTCTAC 61
Db	1 GCACGGGAGCTGTGAGGACGTGTGTGTGTCTCGCTCGGACCTCTTTTCTCTAC 60
QY	62 TGAGATTCACTCTGTGAAATATGAGTTGGCGAGAGATCGACCTATTATTGGCCTAGA 121
Db	61 TGAGATTCACTCTGTGAAATATGAGTTGGCGAGAGATCGACCTATTATTGGCCTAGA 120
QY	122 CCAAGGCGCTATGTACAGCCTCTCTGAAATGATTTGGGCTATGCGGCCGAGCAGTTCACT 181
Db	121 CCAAGGCGCTATGTACAGCCTCTCTGAAATGATTTGGGCTATGCGGCCGAGCAGTTCACT 180
QY	182 GATGAAGTGGAAACACAGCAACACCTGAAAGAGGGGAAACAGCAACTCAACGTCAGGATCCT 241
Db	181 GATGAAGTGGAAACACAGCAACACCTGAAAGAGGGGAAACAGCAACTCAACGTCAGGATCCT 240
QY	242 GCACCTGCTCAGGAGGAGAGGATGAGGAGCATCTGAGGTCAAGGCGGAGGCTGAA 301
Db	241 GCACCTGCTCAGGAGGAGAGGATGAGGAGCATCTGAGGTCAAGGCGGAGGCTGAA 300
QY	302 GCTATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGAT 361
Db	301 GCTATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGAT 360
QY	362 GGGCAGGAGATGGACCCGCCAAATCCAGAGGAGTGAAACCGCTGAAAGAGGTGAAAG 421
Db	361 GGGCAGGAGGTGGACCCGCCAAATCCAGAGGAGTGAAACCGCTGAAAGAGGTGAAAG 420
QY	422 CAATCAGAGTGTAAAGAGGACGTTGAAATGATGAGGCTGCTCTATGTTGAAAT 481
Db	421 CAATCAGAGTGTAAAGAGGACGTTGAAATGATGAGGCTGCTCTATGTTGAAAT 480
QY	482 TTGTTTCAATTAATTTCTCCCAATAAAGCTTTACAGCCTTTCTGCAAAAAA 540
Db	481 TTGTTTCAATTAATTTCTCCCAATAAAGCTTTACAGCCTTTCTGCAAAAAA 539
RESULT 3	
AAAX90522	
ID	AAAX90522 standard; cDNA; 532 BP.
XX	
AC	AAAX90522;
XX	
DT	30-SEP-1999 (first entry)
XX	
DE	GAGE-5 tumour rejection antigen clone nucleotide sequence.
XX	
KW	Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection;
KW	therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;
KW	GAGE; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO9937665-A1.
XX	
PD	29-JUL-1999.
XX	
PF	12-JAN-1999; 99WO-US000775.
XX	
PR	23-JAN-1998; 98US-00012818.
XX	
PA	(LUDW-) LUDWIG INST CANCER RES.
XX	
PI	Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Falleur T;
XX	
DR	WPI; 1999-469111/39.
XX	
PT	New isolated peptides which bind to HLA-A29 molecules, which are tumor

PT	rejection antigens used for detection and therapy of pathological conditions, e.g. cancer.
PT	
XX	Example 13; Fig 4; 62pp; English.
PS	
XX	The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic T lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present invention
XX	
SQ	Sequence 540 BP; 159 A; 113 C; 157 G; 111 T; 0 U; 0 Other;
CC	Query Match 98.9%; Score 534.2; DB 2; Length 540;
CC	Best Local Similarity 99.4%; Pred. No. 7.7e-143; Indels 0; Gaps 0;
CC	Matches 536; Conservative 0; Mismatches 3;
QY	2 GCACGGGAGCTGTGAGGACGTGTGTGTGTCTCGCTCGGACCTCTTTTCTCTAC 61
Db	1 GCACGGGAGCTGTGAGGACGTGTGTGTGTCTCGCTCGGACCTCTTTTCTCTAC 60
QY	62 TGAGATTCACTCTGTGAAATATGAGTTGGCGAGAGATCGACCTATTATTGGCCTAGA 121
Db	61 TGAGATTCACTCTGTGAAATATGAGTTGGCGAGAGATCGACCTATTATTGGCCTAGA 120
QY	122 CCAAGGCGCTATGTACAGCCTCTCTGAAATGATTTGGGCTATGCGGCCGAGCAGTTCACT 181
Db	121 CCAAGGCGCTATGTACAGCCTCTCTGAAATGATTTGGGCTATGCGGCCGAGCAGTTCACT 180
QY	182 GATGAAGTGGAAACACAGCAACACCTGAAAGAGGGGAAACAGCAACTCAACGTCAGGATCCT 241
Db	181 GATGAAGTGGAAACACAGCAACACCTGAAAGAGGGGAAACAGCAACTCAACGTCAGGATCCT 240
QY	242 GCACCTGCTCAGGAGGAGAGGATGAGGAGCATCTGAGGTCAAGGCGGAGGCTGAA 301
Db	241 GCACCTGCTCAGGAGGAGAGGATGAGGAGCATCTGAGGTCAAGGCGGAGGCTGAA 300
QY	302 GCTATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGAT 361
Db	301 GCTATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGAT 360
QY	362 GGGCAGGAGATGGACCCGCCAAATCCAGAGGAGTGAAACCGCTGAAAGAGGTGAAAG 421
Db	361 GGGCAGGAGGTGGACCCGCCAAATCCAGAGGAGTGAAACCGCTGAAAGAGGTGAAAG 420
QY	422 CAATCAGAGTGTAAAGAGGACGTTGAAATGATGAGGCTGCTCTATGTTGAAAT 481
Db	421 CAATCAGAGTGTAAAGAGGACGTTGAAATGATGAGGCTGCTCTATGTTGAAAT 480
QY	482 TTGTTTCAATTAATTTCTCCCAATAAAGCTTTACAGCCTTTCTGCAAAAAA 540
Db	481 TTGTTTCAATTAATTTCTCCCAATAAAGCTTTACAGCCTTTCTGCAAAAAA 539
RESULT 3	
AAAX90522	
ID	AAAX90522 standard; cDNA; 532 BP.
XX	
AC	AAAX90522;
XX	
DT	30-SEP-1999 (first entry)
XX	
DE	GAGE-6 tumour rejection antigen clone nucleotide sequence.
XX	
KW	Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection;
KW	therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;
KW	GAGE; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO9937665-A1.
XX	
PD	29-JUL-1999.
XX	
PF	12-JAN-1999; 99WO-US000775.
XX	
PR	23-JAN-1998; 98US-00012818.
XX	
PA	(LUDW-) LUDWIG INST CANCER RES.
XX	
PI	Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Falleur T;
XX	
DR	WPI; 1999-469111/39.
XX	
PT	New isolated peptides which bind to HLA-A29 molecules, which are tumor



PT agent to be tested for anti-neoplastic activity, and determining a change  
PT in expression of a gene of a signature gene set.  
XX  
PS Claim 1; SEQ ID NO 4660; 44pp; English.

XX The present invention describes a method (M1) for screening for an anti-  
CC neoplastic agent. The method involves exposing cells to a chemical agent  
CC to be tested for anti-neoplastic activity, determining a change in  
CC expression of at least one gene (I) of a signature gene set, where (I)  
CC comprises a sequence (S) selected from 8447 sequences (given in ABU61664  
CC to ABU70110), or is at least 95% identical to (S), where a change in  
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic  
CC activity and can be used in gene therapy. M1 can be used for screening an  
CC anti-neoplastic agent, and can be used for producing a product which is  
CC the data collected with respect to the anti-neoplastic agent as a result  
CC of M1, and the data is sufficient to convey the chemical structure and/or  
CC properties of the agent. M1 can be used in the treatment of cancer such  
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,  
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell  
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous  
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms's  
CC tumour

XX SQ Sequence 528 BP; 147 A; 114 C; 156 G; 111 T; 0 U; 0 Other;

Query Match 97.8%; Score 528; DB 6; Length 528;  
Best Local Similarity 100.0%; Pred. No. 4.5e-141;  
Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCAGGAGCTGTGAGGCACTGCTGTGTCTTCCCGTCGCGACTTTTTCCTCTA 60  
Db 1 CGCCAGGAGCTGTGAGGCACTGCTGTGTCTTCCCGTCGCGACTTTTTCCTCTA 60  
Qy 61 CTGAGATTCATCTGTGTAATATGAGTTGGCGAGGAGATCGACCTATTATTGGCCTAG 120  
Db 61 CTGAGATTCATCTGTGTAATATGAGTTGGCGAGGAGATCGACCTATTATTGGCCTAG 120  
Qy 121 ACCAAGCGCTATGTACAGCTCTCTGAAATGATTGGGCTATGGCGCCGAGCAGTTTCAG 180  
Db 121 ACCAAGCGCTATGTACAGCTCTCTGAAATGATTGGGCTATGGCGCCGAGCAGTTTCAG 180  
Qy 181 TGATGAAGTGAACACAGCAACCTGTAAGAGGGGAAACCACTCAAGCTCAGGATCC 240  
Db 181 TGATGAAGTGAACACAGCAACCTGTAAGAGGGGAAACCACTCAAGCTCAGGATCC 240  
Qy 241 TGCAGCTGCTCAGAGGAGGAGGATGAGGAGCATCTGCAGTCAAGGCGGAGCCTGA 300  
Db 241 TGCAGCTGCTCAGAGGAGGAGGATGAGGAGCATCTGCAGTCAAGGCGGAGCCTGA 300  
Qy 301 AGCTGATAGCCAGGAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGA 360  
Db 301 AGCTGATAGCCAGGAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGA 360  
Qy 361 TGGCAGAGATGAGACCGCCCAATCCAGAGAGGTGAACCGCTGAAGAGGTGAAA 420  
Db 361 TGGCAGAGATGAGACCGCCCAATCCAGAGAGGTGAACCGCTGAAGAGGTGAAA 420  
Qy 421 GCAATCACAGTGTAAAGAGGACCGTTGAAATGATGAGGCTGCTCTATGTGAAA 480  
Db 421 GCAATCACAGTGTAAAGAGGACCGTTGAAATGATGAGGCTGCTCTATGTGAAA 480  
Qy 481 TTTGTTTCAAAAATTTCTCCCAATAAAGCTTTTACAGCCTTTCTGCAAAA 528  
Db 481 TTTGTTTCAAAAATTTCTCCCAATAAAGCTTTTACAGCCTTTCTGCAAAA 528

RESULT 5

AAV18721

XX ID AAV18721 standard; cDNA; 539 BP.

XX AC AAV18721;

XX 30-JUL-1998 (first entry)

XX cDNA encoding GAGE-6 tumour rejection antigen precursor.  
DE  
XX  
KW GAGE tumour rejection antigen precursor; TRAP; tumour; diagnosis;  
KW melanoma; antigen; cytolytic T cell clone proliferation;  
KW HLA-typing assay; ss.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
CDS 82..436  
FT /\*tag= a  
FT /transl\_except= (pos:127..129, aa:Arg)  
FT /transl\_except= (pos:196..198, aa:Ala)  
FT /transl\_except= (pos:199..201, aa:Thr)  
XX  
XX M09749417-A1.  
PN  
XX  
XX 31-DEC-1997.  
PD  
XX  
XX 23-JUN-1997; 97WC-US010850.  
PF  
XX  
XX 24-JUN-1996; 96US-00669161.  
PR  
XX (LUDW-) LUDWIG INST CANCER RES.  
PA  
XX  
XX Debacker O, Van Den Bynde B, Boon-Falleur T;  
PI  
XX  
XX WPI; 1998-076905/07.  
DR P-PSDB; AAW47603.  
XX  
XX  
PT Isolated nucleic acid encoding GAGE tumour rejection antigen precursor -  
PT processed by HLA-Cw6 molecules into peptides, useful to diagnose  
PT melanomas.  
XX  
XX Example 13; Fig 4; 60pp; English.  
XX  
CC The present sequence encodes a GAGE-6 tumour rejection antigen  
CC precursor (TRAP). The protein is expressed in a number of tumours. In  
CC contrast the only normal tissue which expresses GAGE TRAP protein is  
CC testis. Several GAGE TRAPs have been identified (see AAV18717-21). The  
CC major difference between these proteins and GAGE-1 (AAV05540) is the  
CC absence of a stretch of 143 bases located at position 379 to 521 of the  
CC GAGE-1 TRAP sequence. The rest of the sequences show mismatches at  
CC various position, with the exception of GAGE-3 whose 5' end is totally  
CC different from the other GAGE cDNAs for the first 112 bases. This region  
CC of GAGE-3 cDNA contains a long repeat and a hairpin structure. The  
CC antigens can be used to diagnose melanomas, characterised by expression  
CC of a TRAP or presentation of a tumour rejection antigen. Antigens shed  
CC into blood or urine can be observed and then used to confirm a diagnosis  
CC of melanoma using cytolytic T cell clone proliferation methodologies.  
CC Other uses for the processed peptides, include HLA-typing assays for,  
CC e.g. skin graft or organ transplants

XX SQ Sequence 539 BP; 157 A; 114 C; 157 G; 111 T; 0 U; 0 Other;

Query Match 97.1%; Score 524.6; DB 2; Length 539;

Best Local Similarity 98.3%; Pred. No. 4.4e-140;

Matches 530; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 2 GCACGGAGCTGTGAGGCACTGCTGTGTGTTCTGCGCTCGGACTCTTTTCTCTAC 61  
Db 1 GCCAGGAGCTGTGAGGCACTGCTGTGTGTTCTGCGCTCGGACTCTTTTCTCTAC 60

Qy 62 TGAGATTCATCTGTGTAATATGAGTTGGCGAGGAGATCGACTATTATTGGCCTAGA 121

Db 61 TGAGATTCATCTGTGTAATATGAGTTGGCGAGGAGATCGACTATTATTGGCCTAGA 120

Qy 122 CCAAGGCGCTATGTACAGCCTCTCTGAAATGATTGGGCTATGCGGCCGAGCAGTTCACT 181

Db 121 CCAAGGCGCTATGTACAGCCTCTCTGAAATGATTGGGCTATGCGGCCGAGCAGTTCACT 180

Qy 182 GATGAAGTGAACCAACAGCAACACCTGAAGAGGGGAAACCACTCAACGTCAGGATCCT 241



PR 18-APR-2001; 2001US-0284770P.  
 PR 10-MAY-2001; 2001US-0290492P.  
 PR 09-NOV-2001; 2001US-0339245P.  
 PR 13-NOV-2001; 2001US-0350666P.  
 PR 29-NOV-2001; 2001US-0334370P.  
 PR 12-APR-2002; 2002US-0372246P.  
 XX (EOSB-) EOS BIOTECHNOLOGY INC.  
 PA Aziz N, Murray R;  
 XI WPI: 2003-093161/08.  
 XX P-PSDB; ABU56512.  
 DR Detecting a lung cancer-associated transcript in a cell from a patient  
 PT for treating lung cancer, by contacting a biological sample from the  
 PT patient with a polynucleotide that exhibits increased or decreased  
 PT expression in lung cancer.  
 XX Claim 22; Page 273; 453pp; English.  
 XX The invention relates to a method for detecting a lung cancer-associated  
 CC transcript in a cell from a patient, comprising contacting a biological  
 CC sample from the patient with a polynucleotide that selectively hybridises  
 CC to a sequence that is at least 80 % identical to a gene that exhibits  
 CC increased or decreased expression in lung cancer samples. Lung cancer-  
 CC associated polynucleotides and polypeptides are used for identifying a  
 CC compound that modulates a lung cancer-associated polypeptide, for  
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung  
 CC cancer in a patient and for treating a mammal having lung cancer by  
 CC administering a modulatory compound identified. The methods are useful  
 CC for treating lung cancer, such as small cell lung cancer, non-small cell  
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,  
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,  
 CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and  
 CC bronchiectasis. The genes, polynucleotides and polypeptides are useful  
 CC for diagnostic purposes and as targets for screening for therapeutic  
 CC compounds that modulate lung cancer, such as antibodies. Sequences  
 CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the  
 CC invention  
 XX Sequence 527 BP; 146 A; 113 C; 157 G; 111 T; 0 U; 0 Other;

Query Match 96.7%; Score 522.2; DB 7; Length 527;  
 Best Local Similarity 99.4%; Pred. No. 2.1e-139;  
 Matches 524; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 GCCAGGAGCTGTGAGGAGTGTCTGTGGTTCCTGCGCTCGGACTCTTTTCTCTAC 61  
 DB 1 GCCAGGAGCTGTGAGGAGTGTCTGTGGTTCCTGCGCTCGGACTCTTTTCTCTAC 60  
 QY 62 TGAGATTCTCTGTGAAATATGAGTTGGCGAGGAGATCGACCTATTATTGGCTAGA 121  
 DB 61 TGAGATTCTCTGTGAAATATGAGTTGGCGAGGAGATCGACCTATTATTGGCTAGA 120  
 QY 122 CCAAGGCCATATGACACCTCTCTGAATGATGGGCTATGCGGCCCGAGAGTTAGT 181  
 DB 121 CCAAGGCCCTATGTACACCTCTCTGAATGATGGGCTATGCGGCCCGAGAGTTAGT 180  
 QY 182 GATGAAGTGGAAACCAAGCAACCTGAAGAGGGGAACAGCAACTCAAGCTCAGATCCT 241  
 DB 181 GATGAAGTGGAAACCAAGCAACCTGAAGAGGGGAACAGCAACTCAAGCTCAGATCCT 240  
 QY 242 GCAGTGTCTAGGAGGAGAGATGAGGAGCATCTGAGGTCGAAGGCCCGAAGCCTGAA 301  
 DB 241 GCAGTGTCTAGGAGGAGAGATGAGGAGCATCTGAGGTCGAAGGCCCGAAGCCTGAA 300  
 QY 302 GCTGATAGCCAGGACAGGTCACCCAGAGTGGTGTGAGTGAAGATGGTCTGAT 361  
 DB 301 GCTGATAGCCAGGACAGGTCACCCAGAGTGGTGTGAGTGAAGATGGTCTGAT 360  
 QY 362 GGGCAGGAGATGGACCCGCCCAATCCAGAGGAGGTGAAACCGCTGAAGAGGTGAAAG 421

DB 361 GGGCAGGAGGTGGACCCGCCAAATCCAGAGGAGGTGAAACCGCTGAAGAGGTGAAAG 420  
 QY 422 CAATCACAGTGTAAAGAGGACGCTTCAATATGATGAGGCTGCTCTATCTTGAAT 481  
 DB 421 CAATCACAGTGTAAAGAGGACGCTTCAATATGATGAGGCTGCTCTATCTTGAAT 480  
 QY 482 TTGTTTCATTAATAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAAA 528  
 DB 481 TTGTTTCATTAATAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAAA 527

# RESULT 8

AAV18720  
 ID AAV18720 standard; cDNA; 532 BP.  
 XX  
 AC AAV18720;  
 XX  
 DT 30-JUL-1998 (first entry)  
 XX  
 DE cDNA encoding GAGE-5 tumour rejection antigen precursor.  
 XX  
 KW GAGE tumour rejection antigen precursor; TRAP; tumour; diagnosis;  
 KW melanoma; antigen; cytolytic T cell clone proliferation;  
 KW HLA-typing assay; ss.  
 XX  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 CDS 75..429  
 FT /\*tag= a  
 FT /transl\_except= (pos:189..191, aa:Ala)  
 FT /transl\_except= (pos:192..194, aa:Thr)  
 XX  
 PN WO9749417-A1.  
 XX  
 PD 31-DEC-1997.  
 XX  
 PF 23-JUN-1997; 97WO-US010850.  
 XX  
 PR 24-JUN-1996; 96US-00669161.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Debacker O, Van Den Eynde B, Boon-Falleur T;  
 XX  
 DR WPI; 1998-076905/07.  
 DR P-PSDB; AAW47602.  
 XX  
 PT Isolated nucleic acid encoding GAGE tumour rejection antigen precursor -  
 PT processed by HLA-Cw6 molecules into peptides, useful to diagnose  
 PT melanomas.  
 XX  
 PS Example 13; Fig 4; 60pp; English.  
 XX  
 CC The present sequence encodes a GAGE-5 tumour rejection antigen  
 CC precursor (TRAP). The protein is expressed in a number of tumours. In  
 CC contrast the only normal tissue which expresses GAGE TRAP protein is  
 CC testis. Several GAGE TRAPs have been identified (see AAV18717-21). The  
 CC major difference between these proteins and GAGE-1 (AAV05540) is the  
 CC absence of a stretch of 143 bases located at position 379 to 521 of the  
 CC GAGE-1 TRAP sequence. The rest of the sequences show mismatches at  
 CC various positions, with the exception of GAGE-3 whose 5' end is totally  
 CC different from the other GAGE cDNAs for the first 112 bases. This region  
 CC of GAGE-3 cDNA contains a long repeat and a hairpin structure. The  
 CC antigens can be used to diagnose melanomas, characterised by expression  
 CC of a TRAP or presentation of a tumour rejection antigen. Antigens shed  
 CC into blood or urine can be observed and then used to confirm a diagnosis  
 CC of melanoma using cytolytic T cell clone proliferation methodologies.  
 CC Other uses for the processed peptides, include HLA-typing assays for,  
 CC e.g. skin graft or organ transplants  
 XX  
 SQ Sequence 532 BP; 154 A; 110 C; 156 G; 112 T; 0 U; 0 Other;

Query Match	96.4%;	Score 520.8;	DB 2;	Length 532;
Best Local Similarity	98.7%;	Pred. No. 5.3e-139;		
Matches 525;	Conservative	0;	Mismatches 7;	Indels 0;
0;	Gaps	0;		
QY	9	AGCTGTGAGGCGAGTGTCTGTGTGTTCTCTGCGGTCCGGACTCTTTTTCCTCTACTGAGATT	68	
DB	1	AGCTGTGAGGCGAGTGTCTGTGTGTTCTCTGCGGTCCGGACTCTTTTTCCTCTACTGAGATT	60	
QY	69	CATCTGTGTGAAATATGAGTGTGGCGAGGAGATCGACCTATTATTGGCTTACCAAGGC	128	
DB	61	CATCTGTGTGAAATATGAGTGTGGCGAGGAGATCGACCTATTATTGGCTTACCAAGGC	120	
QY	129	GCTATGTACAGCTCTCTGAAATGANTTGGCCCTATGCGCCCGAGCAGTTTCAGTGATGAAG	188	
DB	121	GCTATGTACAGCTCTCTGAAATGANTTGGCCCTATGCGCCCGAGCAGTTTCAGTGATGAAG	180	
QY	189	TGGAACCAAGCAACCTGTAAGAGGGAACCAAGCAACTCAAGTCAAGATCTGAGCTG	248	
DB	181	TGGAACCAAGCAACCTGTAAGAGGGAACCAAGCAACTCAAGTCAAGATCTGAGCTG	240	
QY	249	CTCAGGAGGAGAGATGAGGAGCATCTGCAGGTCAAGGGCCGAAGCTCAAGCTGATA	308	
DB	241	CTCAGGAGGAGAGATGAGGAGCATCTGCAGGTCAAGGGCCGAAGCTCAAGCTGATA	300	
QY	309	GCCAGGACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGCAGG	368	
DB	301	GCCAGGACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGCAGG	360	
QY	369	AGATGGACCCGCAAAATCCAGAGGAGGTGAAAACCCCTGGAAGAGGTGAAAAGCAATCAC	428	
DB	361	AGATGGACCCGCAAAATCCAGAGGAGGTGAAAACCCCTGGAAGAGGTGAAAAGCAATCAC	420	
QY	429	AGTGTGTTAAAGAGGAGGAGTGAATGATGAGGCTGCTCTATGTTGGAAATTTGTTCA	488	
DB	421	AGTGTGTTAAAGAGGAGGAGTGAATGATGAGGCTGCTCTATGTTGGAAATTTGTTCA	480	
QY	489	TTAAATTTCTCCATAAAGCTTTACAGCTTCTGCAAAAAAAGAAAAA	540	
DB	481	TTAAATTTCTCCATAAAGCTTTACAGCTTCTGCAAAAAAAGAAAAA	532	
RESULT 9				
AAX90519				
ID	AAX90519	standard; cdNA; 538 BP.		
XX	AC	AAX90519;		
XX	DT	30-SEP-1999 (first entry)		
XX	XX	GAGE-2 tumour rejection antigen clone nucleotide sequence.		
XX	DE	Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection;		
XX	KW	therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;		
XX	KW	GAGE; ss.		
OS	OS	Homo sapiens.		
XX	PN	WO9937665-A1.		
XX	PD	29-JUL-1999.		
XX	XX	12-JAN-1999; 99WO-US000775.		
XX	PF	23-JAN-1998; 98US-00012818.		
XX	PR	(LUDW-) LUDWIG INST CANCER RES.		
XX	PA	Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Falleur T;		
XX	PI	WPI; 1999-469111/39.		
XX	DR	New isolated peptides which bind to HLA-A29 molecules, which are tumor		
XX	PT	rejection antigens used for detection and therapy of pathological		







```

DE cDNA encoding GAGE-2 tumour rejection antigen precursor.
XX
KW GAGE tumour rejection antigen precursor; TRAP; tumour; diagnosis;
KW melanoma; antigen; cytolytic T cell clone proliferation;
KW HLA-typing assay; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 81..431
FT /*tag= a
FT /transl_except= (pos:192..194, aa:Ala)
FT /transl_except= (pos:195..197, aa:Thr)
XX
XX WO9749417-A1.
XX
XX 31-DEC-1997.
XX
XX 23-JUN-1997; 97WO-US010850.
XX
XX 24-JUN-1996; 96US-00669161.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Debacker O, Van Den Eynde B, Boon-Falleur T;
XX
XX WPI; 1998-076905/07.
XX
XX P-PSDB; AAW47599.
XX
XX Isolated nucleic acid encoding GAGE tumour rejection antigen precursor -
XX processed by HLA-Cw6 molecules into peptides, useful to diagnose
XX melanomas.
XX
XX Example 13; Fig 4; 60pp; English.
XX
XX The present sequence encodes a GAGE-2 tumour rejection antigen
XX precursor (TRAP). The protein is expressed in a number of tumours. In
XX contrast the only normal tissue which expresses GAGE TRAP protein is
XX testis. Several GAGE TRAPs have been identified (see AAV18717-21). The
XX major difference between these proteins and GAGE-1 (AAV05540) is the
XX absence of a stretch of 143 bases located at position 379 to 521 of the
XX GAGE-1 TRAP sequence. The rest of the sequences show mismatches at
XX various position, with the exception of GAGE-3 whose 5' end is totally
XX different from the other GAGE cDNAs for the first 112 bases. This region
XX of GAGE-3 cDNA contains a long repeat and a hairpin structure. The
XX antigens can be used to diagnose melanomas, characterised by expression
XX into a TRAP or presentation of a tumour rejection antigen. Antigens shed
XX into blood or urine can be observed and then used to confirm a diagnosis
XX of melanoma using cytolytic T cell clone proliferation methodologies.
XX Other uses for the processed peptides, include HLA-typing assays for,
XX e.g. skin graft or organ transplants
XX
XX Sequence 535 BP; 158 A; 112 C; 156 G; 109 T; 0 U; 0 Other;
XX
XX Query Match 87.2%; Score 471; DB 2; Length 535;
XX Best Local Similarity 95.7%; Pred. No. 1e-124;
XX Matches 518; Conservative 0; Mismatches 15; Indels 8; Gaps 3;
XX
XX 1 CGCCAGGGAGCTGTGAGGAGTGTGTGTGTTCTTCGTCGTCGAGTCTTTTCCTC-T 59
XX
XX 2 CGCCAGGGAGCTGTGAGGAGTGTGTGTGTTCTTCGTCGTCGAGTCTTTTCCTC-T 57
XX
XX 60 ACTGAGATTCATCTGTGTAAATATGAGTTGGCGAGGAGATCGACTATATTGGCTTA 119
XX
XX 58 ACTGAGATTCATCTGTGTAAATATGAGTTGGCGAGGAGATCGACTACCC---TATCGGCTTA 114
XX
XX 120 GACCAGGGCTATGTACAGCCCTCTGAAATGATTGGGCTATGGCGCCGAGCAGTTCA 179
XX
XX 115 GACCAAGAGCTACGTAGACCCCTCTGAAATGATTGGGCTATGGCGCCGAGCAGTTCA 174
XX
XX 180 GTGATCAAGTGGAAACAGCAACACCTTGAAGAGGGGAACACGACCACTCAACGTCAGGATC 239
XX
XX 175 GTGATCAAGTGGAAACAGCAACACCTTGAAGAGGGGAACACGACCACTCAACGTCAGGATC 234

```

```

QY 240 CTCGAGCTGCTCAGGAGGAGAGATGAGGAGAGCATCTGAGGTCAAGGCCGAGGCTG 299
DB 235 CTGAGCTGCTCAGGAGGAGAGATGAGGAGAGCATCTGAGGTCAAGGCCGAGGCTG 294
QY 300 AAGCTGATAGCCAGGAACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTG 359
DB 295 AAGTGTAGAGCCAGGAACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTG 354
QY 360 ATGGGAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAACGCCCTGAAAGAGGTGAAA 419
DB 355 ATGGGAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAACGCCCTGAAAGAGGTGAAA 414
QY 420 AGCAATCACAGTGTATAAAGAGGACGCTTGAATGATGAGGCTGCTCTATGTTGAA 479
DB 415 AGCAATCACAGTGTATAAAGAGGACATGTTGAATGATGAGGCTGCTCTATGTTGAA 474
QY 480 ATTGTTTCATTAAATTCCTCCCAATAAAGCTTTACAGCCTTTCTGCAAAAAA 539
DB 475 ATTGTTTCATTAAATTCCTCCCAATAAAGCTTTACAGCCTTTCTGCAAAAAA 534
QY 540 A 540
DB 535 A 535

```

## RESULT 14

AAC02129

ID AAC02129 standard; cDNA; 430 BP.

XX AAC02129;

XX 06-OCT-2000 (first entry)

XX Human secreted protein 5' EST, SEQ ID NO: 2127.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.

XX Homo sapiens.

XX EF1033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

XX (GEST ) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

XX P-PSDB; AAG02123.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX Claim 1; SEQ ID NO 2127; 71pp + Sequence Listing; English.

XX The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,

CC	gene therapy and chromosome mapping procedures. They are used to obtain
CC	upstream regulatory sequences and to design expression and secretion
CC	vectors
XX	
SQ	Sequence 430 BP; 101 A; 102 C; 134 G; 85 T; 0 U; 8 Other;
	Query Match 66.7%; Score 360.4; DB 3; Length 430;
	Best Local Similarity 97.9%; Pred. No. 4.9e-93;
	Matches 369; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
QY	1 CGCCAGGAGCTGTGAGGCAGTCTGTGGTTTCCTGCCGTCGCGACTCTTTTCCTCTA 60
DB	55 CGCCAGGAGCTGTGAGGCAGTCTGTGGTTTCCTGCCGTCGCGACTCTTTTCCTCTA 114
QY	61 CTGAGATTCAATCTGTGAAATATGAGTTGGCAGGAAGATCGACCTATTATTGGCCCTAG 120
DB	115 CTGAGATTCAATCTGTGAAATATGAGTTGGCAGGAAGATCGACCTATNA-YGGCCTAG 173
QY	121 ACCAAGCGCTATGTACAGCCTCCTGAAATGATTGGGCCTATGGGCCCGAGCAGTTGAG 180
DB	174 ACCAAGRCGCTATGTACAGCCTCCTGAAATGATTGGGCCTATGGGCCCGAGCAGTTGAG 233
QY	181 TGATGAAGTGGAACACAGCACCTGAAGAGGGGACCACGAACTCAACCTCAGGATCC 240
DB	234 TGATGAAGTGGAAACACAGCACCTGAAGAGGGGAAACGCAACTCAAYGTTCAGGATCC 293
QY	241 TGCAGCTGCTCAGGAGGAGAGGATGAGGGAGCATCTGCAGTCAAGGCGCCGAAAGCCTGA 300
DB	294 TGCAGCTGCTCAGRAGGAGAGGATGAGGGAGCATCTGCAGTCAAGGCGCCGAAAGCCTGA 353
QY	301 AGCTGATAGCCAGGAACAAGGGTCAACCCACAGACTGGGTGTGAGTGTAAGATGGTCTCTGA 360
DB	354 AGCTCATAGCCAGGAACAAGGGTCAACCCACAGACTGGGTGTGAGTGTAAGATGGTCTCTGA 413
QY	361 TGGCAGGAGATGGACC 377
DB	414 TGGCAGGAGATGGAMC 430
RESULT 15	
AAS60104/c	ID AAS60104 standard; cDNA; 530 BP.
XX	AAS60104;
XX	
DT	29-JAN-2002 (first entry)
XX	Human cancer agent-sensitive marker #105.
XX	Human; cancer cell marker; TAXOL; cytostatic; tumour; carcinoma;
KW	squamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia;
KW	lymphocytic leukaemia; lymphoma; plasmacytoma; reticulum cell sarcoma;
KW	Hodgkin's disease; glioma; ss.
OS	Homo sapiens.
XX	
PN	WO200179556-A2.
XX	
PD	25-OCT-2001.
XX	
PF	13-APR-2001; 2001WO-USO12132.
XX	
PR	14-APR-2000; 2000US-0197538P.
XX	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA	Lillie J, Brown JL, Bolt A, Van Huffel C;
PI	
XX	WPI; 2001-602933/68.
DR	
XX	
PT	Novel nucleic acid, used as a marker to determine the effectiveness of
XX	using TAXOL to treat cancer cell growth in individuals.
XX	

Claim 1; Page 120; 527pp; English.

The invention relates to 1046 novel nucleic acids which are used as markers for determining the sensitivity of a cancer cell to the anticancer agent TAXOL. Cancer cells can be treated with TAXOL when they are shown to express one of the 242 sensitivity markers or the cells are shown not to express one of the 804 resistance markers. The methods can be used to determine the effectiveness of TAXOL in the treatment of cancer cell growth in an individual. The markers can be used as targets in developing anti-cancer agents such as chemotherapeutic compounds. The markers can also be used as targets in developing treatments for cancer, particularly those cancers which display resistance to agents and exhibit expression of the markers. The anticancer agents developed by the novel method can be used to treat cancer. Probes based on the markers can be used to detect transcripts or genomic sequences corresponding to the markers, in the identification of cells or tissues which mis-express the protein. Cancers which may be targeted include carcinoma (e.g. squamous cell carcinoma), sarcoma (e.g. fibrosarcoma) leukaemia (e.g. lymphocytic leukaemia), lymphoma, plasmacytoma, reticulom cell sarcoma, Hodgkin's disease and tumours (e.g. glioma). The present sequence is one of the 1046 novel cancer cell markers

Sequence 530 BP; 89 A; 100 C; 106 G; 183 T; 0 U; 52 Other;

Query Match 56.7%; Score 306.2; DB 4; Length 530;  
Best Local Similarity 88.7%; Pred. No. 1.9e-77;  
Matches 323; Conservative 0; Mismatches 39; Indels 2; Gaps 1;

QY 179 AGTGATGAAGTGGAAACCAGC--ACACCTGAAGAGGGGACACAGCAACTCAAGCTCAGG 236  
DB 449 AGTATNAAGTGGACCCANCCNCCCTGHAANAAGGNAACACAGCAACTCAAGTNAGG 390  
QY 237 ATCTGTGCAGCTGCTCAGGAGGAGGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGC 296  
DB 389 ATCTGNAGTGCNCAGNAGGAGNAGGATNAGGNGCATNTGTCAGGTCAAGGGCCGAAGC 330  
QY 297 CTGAAGCTGTATAGCCAGAAACAGGGTCAACCCACAGACTGGGTGTGACGTGTCAGATGTCGTC 356  
DB 329 CTGAAGNTGATAGCCAGGAACAGGGTCTNCCGCCCACTGGGNGTNAAGTGTGTTAAATGGTC 270  
QY 357 CTGATGGCCAGAGATGACCCGCCAAATCCAGAGGAGGTGAAACCGCTCGAAGAAGGTG 416  
DB 269 CTNATGGGCAGNANATGACCCNCCAATCCAAAGNAGGTGAAACNCCTGAANAAGGTG 210  
QY 417 AAAAGCAATCAAGTGTGTTAAAGAGGACGCGTTGAAATGATGTCAGGCTGCTCCTATGTTG 476  
DB 209 AAAAGCAATCCAGTGTGTTAAANAAGGNCGTTGAAATGATGTCAGGCTGCTCCTATGTTG 150  
QY 477 GAAATTTGTTCAATTAATAATCTCCCAATAAAGCTTTTACAGCCTTCTGCAAAAAAATAAAA 536  
DB 149 GAAATTTGTTCAATTAATAATCTCCCAATAAAGCTTTTACAGCCTTNTNAAAAAATAAAA 90  
QY 537 AAAA 540  
DB 89 AAAA 86

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Job time : 342 secs

Search completed: August 6, 2004, 17:02:11  
Job time : 342 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 19:14:51 ; Search time 2249 Seconds  
(without alignments)  
10252.776 Million cell updates/sec

Title: US-09-782-745-17

Perfect score: 532

Sequence: 1 AGCTGTGAGGCAGTGTGTG.....CTGCAGAGAAAAA 532

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 3957288

Minimum DB seq length: 0

Maximum DB seq length: 532

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: gb\_pat.\*  
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8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
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26: em\_sts.\*  
27: em\_un.\*  
28: em\_vi.\*  
29: em\_vl.\*  
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40: em\_hrgo\_mus.\*  
41: em\_hrgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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1	532	100.0	532	6	AR028491	AR028491 Sequence
2	532	100.0	532	6	BD231800	BD231800 Isolated
3	532	100.0	532	6	I55854	I55854 Sequence 17
4	532	100.0	532	6	BD132470	BD132470 Isolated
5	524	98.5	524	9	HSU19146	U19146 Human GAGE-
6	517.4	97.3	528	6	AX334151	AX334151 Sequence
7	517.4	97.3	528	9	HSU19145	U19145 Human GAGE-
8	515.8	97.0	527	9	HSU19147	U19147 Human GAGE-
9	513.4	96.5	524	9	AF058988	AF058988 Homo sapi
10	508.8	95.6	526	6	AR275666	AR275666 Sequence
11	508.8	95.6	526	9	AF055474	AF055474 Homo sapi
12	504.4	94.8	528	6	AR275665	AR275665 Sequence
13	504.4	94.8	528	9	AF055473	AF055473 Homo sapi
14	496.8	93.4	530	9	HSU19143	U19143 Human GAGE-
15	350.8	65.9	430	6	AX886264	AX886264 Sequence
16	350.8	65.9	430	6	BD025874	BD025874 Sequence
17	304.6	57.3	530	6	AX284300	AX284300 Sequence
18	302.4	56.8	365	6	AX284692	AX284692 Sequence
19	174.2	32.7	493	9	HSU19143	U19143 Human GAGE-
20	171.6	32.3	494	6	AX921771	AX921771 Sequence
21	150.6	28.3	441	12	BT007722	BT007722 Synthetic
22	147.4	27.7	506	6	AR415772	AR415772 Sequence
23	147.4	27.7	506	6	BD111325	BD111325 EST and e
24	136	25.6	494	6	AR416094	AR416094 Sequence
25	136	25.6	494	6	BD111647	BD111647 EST and e
26	133.2	25.0	475	6	AX226497	AX226497 Sequence
27	131.8	24.8	500	9	BC054022	BC054022 Homo sapi
28	128	24.1	524	6	AR416095	AR416095 Sequence
29	128	24.1	524	6	BD111848	BD111848 EST and e
30	118	22.2	448	6	AX226538	AX226538 Sequence
31	111.6	21.0	448	6	AX226537	AX226537 Sequence
32	111.4	20.9	529	9	BC009538	BC009538 Homo sapi
33	108	20.3	399	6	AR272357	AR272357 Sequence
34	108	20.3	399	6	AR275938	AR275938 Sequence
35	108	20.3	399	6	AR406213	AR406213 Sequence
36	108	20.3	399	6	AX062442	AX062442 Sequence
37	108	20.3	399	6	AX367359	AX367359 Sequence
38	104.4	19.6	463	9	HSU290447	U19145 Human GAGE-
39	103.4	19.4	463	6	AX370580	AX370580 Sequence
40	102	19.2	467	9	BC010897	BC010897 Homo sapi
41	101.6	19.1	515	6	BD242364	BD242364 Compounds
42	101.6	19.1	515	6	AR261040	AR261040 Sequence
43	101.6	19.1	515	6	AR278571	AR278571 Sequence
44	101.6	19.1	515	6	AR367267	AR367267 Sequence
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# ALIGNMENTS

RESULT 1  
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LOCUS AR028491 532 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 17 from patent US 5858689.  
ACCESSION AR028491  
VERSION AR028491.1 GI:5940464  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 532)  
AUTHORS van der Bruggen,P., van den Eynde,B., DeBacker,O. and Boon-Falleur,T.  
TITLE Isolated peptides derived from the gage tumor rejection antigen precursor and uses thereof

Pred. No. is the number of results predicted by chance to have a

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JOURNAL Patent: US 5858689-A 17 12-JAN-1999;
FEATURES Location/Qualifiers
source
1. .532
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 532; DB 6; Length 532;
Best Local Similarity 100.0%; Pred. No. 1.5e-127; Indels 0; Gaps 0;
Matches 532; Conservative 0; Mismatches 0;

QY 1 AGCTGTGAGCAGTGTGTGTTCTGCGCTCGGACTCTTTTCTCTACTGAGATT 60
DB 1 AGCTGTGAGCAGTGTGTGTTCTGCGCTCGGACTCTTTTCTCTACTGAGATT 60
QY 61 CATCTGTGTAATATAGTGTGGCAGGAGATCGACTTATTATGGCCCTAGACCAAGGC 120
DB 61 CATCTGTGTAATATAGTGTGGCAGGAGATCGACTTATTATGGCCCTAGACCAAGGC 120
QY 121 GCTATGTACAGCTTCTGAACTGATTTGGGCTATGCGGCCGAGCAGTTCAGTGAAG 180
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DB 241 CTCAGAGGAGAGATGAGGAGCATCTGCAGTCAAGGCGCGAGCTTCAAGCTGATA 300
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RESULT 2
BD231800 532 bp DNA linear PAT 17-JUL-2003
LOCUS Isolated polypeptides binding with HLA-A29 molecule, nucleic acids
DEFINITION as molecules encoding the same, and utilization thereof.
ACCESSION BD231800
VERSION JP 2002509859-A/10.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 532)
AUTHORS Bruggen,P.V.D., Eynde,B.V.D., Debacker,O. and Falleur,T.B.
TITLE Isolated polypeptides binding with HLA-A29 molecule, nucleic acids
as molecules encoding the same, and utilization thereof
JOURNAL Patent: JP 2002509859-A 10 02-APR-2002;
COMMENT LUDWIG INSTITUTE FOR CANCER RESEARCH
OS Homo sapiens (human)
PN JP 2002509859-A/10
PD 02-APR-2002
PF 12-JAN-1999 JP 2000528586
PR 23-JAN-1998 US 09/012818
PI PIERRE VAN DER BRUGGEN,BENOIT VAN DEN EYNDE,OLIVIER DEBACKER,
THIERRY BOON FALLEUR
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PC C07K4/12,C12N15/09,C12P21/00,C12Q1/00,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
CC STRANDEDNESS:single,TOPOLOGY:linear
FH Key Location/Qualifiers
FT source 1. .532
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1. .532
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Query Match 100.0%; Score 532; DB 6; Length 532;
Best Local Similarity 100.0%; Pred. No. 1.5e-127; Indels 0; Gaps 0;
Matches 532; Conservative 0; Mismatches 0;

QY 1 AGCTGTGAGCAGTGTGTGTTCTGCGCTCGGACTCTTTTCTCTACTGAGATT 60
DB 1 AGCTGTGAGCAGTGTGTGTTCTGCGCTCGGACTCTTTTCTCTACTGAGATT 60
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DB 121 GCTATGTACAGCTTCTGAACTGATTTGGGCTATGCGGCCGAGCAGTTCAGTGAAG 180
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QY 241 CTCAGAGGAGAGATGAGGAGCATCTGCAGTCAAGGCGCGAGCTTCAAGCTGATA 300
DB 241 CTCAGAGGAGAGATGAGGAGCATCTGCAGTCAAGGCGCGAGCTTCAAGCTGATA 300
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DB 301 GCCAGGACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGTGTCTTATGTTGGAATTTGTTCA 480
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DB 361 AGATGGACCCGCCAAATCCAGAGAGGTGAAACCGCTCGAAGAGGTGAAAGCAATCAC 420
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QY 481 TTAATAATCTCCCAATAAGCTTTACAGCTTCTGCAAGCAAAAAA 532
DB 481 TTAATAATCTCCCAATAAGCTTTACAGCTTCTGCAAGCAAAAAA 532

RESULT 3
BD231800 532 bp DNA linear PAT 07-OCT-1997
LOCUS Isolated polypeptides binding with HLA-A29 molecule, nucleic acids
DEFINITION as molecules encoding the same, and utilization thereof.
ACCESSION BD231800
VERSION JP 2002509859-A/10.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 532)
AUTHORS Van den Eynde,B., Debacker,O. and Boon-Falleur,T.
TITLE Isolated peptides derived from tumor rejection antigens, and their
use
JOURNAL Patent: US 5648226-A 17 15-JUL-1997;
COMMENT LUDWIG INSTITUTE FOR CANCER RESEARCH
OS Homo sapiens (human)
PN JP 2002509859-A/10
PD 02-APR-2002
PF 12-JAN-1999 JP 2000528586
PR 23-JAN-1998 US 09/012818
PI PIERRE VAN DER BRUGGEN,BENOIT VAN DEN EYNDE,OLIVIER DEBACKER,
THIERRY BOON FALLEUR
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Best Local Similarity		100.0%; Pred. No. 1.5e-127;	
Matches 532; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
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QY	61	CATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGC	120
DB	61	CATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGC	120
QY	121	GCTATGTACAGCCTCTCTGAAGTGAITGGGCCCTATGCGGCCCGAGCAGTTCAGTGAATGAAG	180
DB	121	GCTATGTACAGCCTCTCTGAAGTGAITGGGCCCTATGCGGCCCGAGCAGTTCAGTGAATGAAG	180
QY	181	TGGAACCAACAACCTGGAAGAGGGGAACCACTCAAGTCAAGATCCTGCGAGCTG	240
DB	181	TGGAACCAACAACCTGGAAGAGGGGAACCACTCAAGTCAAGATCCTGCGAGCTG	240
QY	241	CTCAGGAGGAGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATA	300
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DB	301	GCAGGAAACAGGGTCAACCCACAGATGGGTGTGAGTGTGAAGATGCTTGTATGGGCAGG	360
QY	361	AGATGACCCGCCCAATCCAGAGGAGTGAAACGCTCGAGAGGTGAAACCAATCAC	420
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DB	421	AGTGTATAAAGAGGACGTTGAAATGATGAGGCTGCTCCTATGTTGAAAATTGTTC	480
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DB	481	TTAAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA	532
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LOCUS		Human GAGE-5 protein mRNA, complete cds.	
DEFINITION		U19146	
ACCESSION		U19146.1 GI:914906	
VERSION		Homo sapiens (human)	
KEYWORDS		Homo sapiens	
SOURCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
ORGANISM		1 (bases 1 to 524); Van den Eynde, B., Peeters, O., De Backer, O., Gaugler, B., Lucas, S. and Boon, T.	
REFERENCE		A new family of genes coding for an antigen recognized by autologous cytolytic T lymphocytes on a human melanoma	
AUTHORS		J. Exp. Med. 182 (3), 689-698 (1995)	
TITLE		95378788	
JOURNAL		7544395	
MEDLINE		2 (bases 1 to 524)	
PUBMED		Van den Eynde, B.J.	
REFERENCE		Direct Submission	
AUTHORS		Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium	
TITLE		JOURNAL	
JOURNAL		for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium	
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DB	1	AGCTGTGAGGAGTGTCTGTGTGTTCTCGCGTCCGGACTCTTTTCCTCTACTGAGATT	60
QY	61	CATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGC	120
DB	61	CATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGC	120
QY	121	GCTATGTACAGCCTCTCTGAAGTGAITGGGCCCTATGCGGCCCGAGCAGTTCAGTGAATGAAG	180
DB	121	GCTATGTACAGCCTCTCTGAAGTGAITGGGCCCTATGCGGCCCGAGCAGTTCAGTGAATGAAG	180
QY	181	TGGAACCAACAACCTGGAAGAGGGGAACCACTCAAGTCAAGATCCTGCGAGCTG	240
DB	181	TGGAACCAACAACCTGGAAGAGGGGAACCACTCAAGTCAAGATCCTGCGAGCTG	240
QY	241	CTCAGGAGGAGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATA	300
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QY	301	GCAGGAAACAGGGTCAACCCACAGATGGGTGTGAGTGTGAAGATGCTTGTATGGGCAGG	360
DB	301	GCAGGAAACAGGGTCAACCCACAGATGGGTGTGAGTGTGAAGATGCTTGTATGGGCAGG	360
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DB	361	AGATGACCCGCCCAATCCAGAGGAGTGAAACGCTCGAGAGGTGAAACCAATCAC	420
QY	421	AGTGTATAAAGAGGACGTTGAAATGATGAGGCTGCTCCTATGTTGAAAATTGTTC	480
DB	421	AGTGTATAAAGAGGACGTTGAAATGATGAGGCTGCTCCTATGTTGAAAATTGTTC	480
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RESULT 4		BD132470 532 bp DNA linear PAT 18-SEP-2002	
LOCUS		Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof.	
DEFINITION		BD132470	
ACCESSION		BD132470.1 GI:23227415	
VERSION		JP 2002507112-A/10.	
KEYWORDS		synthetic construct	
SOURCE		artificial sequences.	
ORGANISM		1 (bases 1 to 532); Debacker, O., Eynde, B.V.D. and Falleur, T.B.	
REFERENCE		Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof	
AUTHORS		Patent: JP 2002507112-A 10 05-MAR-2002;	
TITLE		LUDWIG INSTITUTE FOR CANCER RESEARCH	
JOURNAL		PN JP 2002507112-A/10	
COMMENT		FD 05-MAR-2002	
PF		23-JUN-1997 JP 1998503430	
PR		24-JUN-1996 US 08/669161	
PI		OLIVIER DEBACKER, BENOIT VAN DEN EYNDE, THIERRY BOON FALLEUR PC A61K38/00, A61K45/05, C07K7/00, C07K14/82, C12N15/00 CC	
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Topology:		Linear;	
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## CDS

## ORIGIN

Query Match 98.5%; Score 524; DB 9; Length 524;  
Best Local Similarity 100.0%; Pred. No. 1.8e-125;  
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTGTGAGGAGTCTGTGTGTTCTCGCTCCGCGACTCTTTTCTCTACTCAGATT 60  
Db 1 AGCTGTGAGGAGTCTGTGTGTTCTCGCTCCGCGACTCTTTTCTCTACTCAGATT 60  
QY 61 CATCTGTGAAATATGATGTTGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGGC 120  
Db 61 CATCTGTGAAATATGATGTTGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGGC 120  
QY 121 GCTATGTACAGCTCTCTGAAGTGATTGGGCTATGCGGCCGAGCAGTTCAGTGATGAAG 180  
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QY 181 TGGAAACAGCAACACCTGAAGTGGGCTATGCGGCCGAGCAGTTCAGTGATGAAG 240  
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QY 241 CTCAGGAGGAGAGATGAGGAGCATCTGCAGGTCAGGCTCAAGGCGGAAAGCAATCAC 300  
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QY 301 GCCAGGAACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGGCGAG 360  
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QY 361 AGATGGACCCGCAAAATCCAGAGGAGGTGAAAGCCCTGGAAGAGGTGAAAGCAATCAC 420  
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QY 421 AGCTGTAAAGAGGACGTTGAAATGATGAGGCTGCTCTATGTTGGAAATTTGTTCA 480  
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QY 481 TTAATAATCTCCCAATAAGCTTTACAGCTTCTGCAAGAAAA 524  
Db 481 TTAATAATCTCCCAATAAGCTTTACAGCTTCTGCAAGAAAA 524

## RESULT 6

AX334151  
LOCUS AX334151 528 bp DNA linear PAT 09-JAN-2002  
DEFINITION Sequence 4660 from Patent WO0194629.  
ACCESSION AX334151  
VERSION AX334151.1 GI:18124870  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ehner,R., Endress,G.,  
Horrikan,S., Soppet,D.R. and Weaver,Z.  
TITLE Cancer gene determination and therapeutic screening using signature  
gene sets  
JOURNAL Patent: WO 0194629-A 4660 13-DEC-2001;

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source Avalon Pharmaceuticals (US)  
Location/Qualifiers  
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Best Local Similarity 99.8%; Pred. No. 9.2e-124;  
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QY 1 AGCTGTGAGGAGTCTGTGTGTTCTCGCTCCGCGACTCTTTTCTCTACTCAGATT 60  
Db 9 AGCTGTGAGGAGTCTGTGTGTTCTCGCTCCGCGACTCTTTTCTCTACTCAGATT 68  
QY 61 CATCTGTGAAATATGATGTTGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGGC 120  
Db 69 CATCTGTGAAATATGATGTTGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGGC 128  
QY 121 GCTATGTACAGCTCTCTGAAGTGATTGGGCTATGCGGCCGAGCAGTTCAGTGATGAAG 180  
Db 129 GCTATGTACAGCTCTCTGAAGTGATTGGGCTATGCGGCCGAGCAGTTCAGTGATGAAG 188  
QY 181 TGGAAACAGCAACACCTGAAGTGGGCTATGCGGCCGAGCAGTTCAGTGATGAAG 240  
Db 189 TGGAAACAGCAACACCTGAAGTGGGCTATGCGGCCGAGCAGTTCAGTGATGAAG 248  
QY 241 CTCAGGAGGAGAGATGAGGAGCATCTGCAGGTCAGGCTCAAGGCGGAAAGCAATCAC 300  
Db 249 CTCAGGAGGAGAGATGAGGAGCATCTGCAGGTCAGGCTCAAGGCGGAAAGCAATCAC 308  
QY 301 GCCAGGAACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGGCGAG 360  
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QY 361 AGATGGACCCGCAAAATCCAGAGGAGGTGAAAGCCCTGGAAGAGGTGAAAGCAATCAC 420  
Db 369 AGATGGACCCGCAAAATCCAGAGGAGGTGAAAGCCCTGGAAGAGGTGAAAGCAATCAC 428  
QY 421 AGCTGTAAAGAGGACGTTGAAATGATGAGGCTGCTCTATGTTGGAAATTTGTTCA 480  
Db 429 AGCTGTAAAGAGGACGTTGAAATGATGAGGCTGCTCTATGTTGGAAATTTGTTCA 488  
QY 481 TTAATAATCTCCCAATAAGCTTTACAGCTTCTGCAAA 519  
Db 489 TTAATAATCTCCCAATAAGCTTTACAGCTTCTGCAAA 527

## RESULT 7

HSU19145  
LOCUS Human GAGE-4 protein mRNA, complete cds.  
DEFINITION U19145  
ACCESSION U19145  
VERSION U19145.1 GI:914904  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Van den Eynde,B., Peeters,O., De Backer,O., Gaugler,B., Lucas,S.  
and Boon,T.  
TITLE A new family of genes coding for an antigen recognized by  
autologous cytolytic T lymphocytes on a human melanoma  
J. Exp. Med. 182 (3), 689-698 (1995)  
MEDLINE 95378788  
PUBMED 754395  
REFERENCE 2 (bases 1 to 528)  
AUTHORS Van den Eynde,B.J.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute  
for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium







AF055474  
LOCUS Homo sapiens GAGE-7B mRNA 526 bp mRNA linear PRI 01-MAY-2000  
DEFINITION Homo sapiens GAGE-7B mRNA, complete cds.  
ACCESSION AF055474  
VERSION AF055474.1 GI:3511024  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 526)  
AUTHORS De Bakker, O., Arden, K.C., Boretti, M., Vantomme, V., De Smet, C.,  
Czekay, S., Viars, C.S., De Plaen, E., Brasseur, F., Chomez, P., Van den  
Eynde, B., Boon, T., and van der Bruggen, P.  
TITLE Characterization of the GAGE genes that are expressed in various  
human cancers and in normal testis  
JOURNAL Cancer Res. 59 (13), 3157-3165 (1999)  
MEDLINE 99323388  
PubMed 10397259  
REFERENCE 2 (bases 1 to 526)  
AUTHORS De Bakker, O.R.Y.  
TITLE Direct Submission  
JOURNAL Submitted (24-MAR-1998) Ludwig Institute for Cancer Research,  
Brussels Branch, 74 av. Hippocrate, Brussels B-1200, Belgium  
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Best Local Similarity 99.6%; Pred. No. 1.6e-121;  
Matches 510; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 21 TGGTCTCTGCGCGGACGCTTTTCTCTACTGAGATTCATCTGTGTAATATGAGT 80  
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QY 81 TGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCTTGAA 140  
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QY 141 GTGATTGGGCTATGCGGCGGAGCAGTTGAGTGAATGAGTGAACAGCAACACCTGAA 200  
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QY 201 GAAGGGGAACAGCAACTCAACGTCAGGATCCTGCTGCTGCTGAGGAGGAGGAGTGA 260  
Db 181 GAAGGGGAACAGCAACTCAACGTCAGGATCCTGCTGCTGCTGAGGAGGAGGAGTGA 240

QY 261 GGAGCATCTGAGGTCGAAGGCGCAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCA 320  
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QY 321 CAGACTGGGTGAGTGTGAAGATGGTCTGATGGGAGGAGATGGACCCGCCAAATCCA 380  
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QY 381 GAGAGGTGAACAGCCTGAAGAGGTGAAGCAATCAAGTCTTTAAAGAGGCGACGT 440  
Db 361 GAGAGGTGAACAGCCTGAAGAGGTGAAGCAATCAAGTCTTTAAAGAGGCGACGT 420

QY 441 TGAATGATGAGGCTGCTCTATGTTGGAATTTGTTTCAATTAATTTCTCCCAATAAG 500

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Db 481 CTTTACAGCCTTCTGCAAGAAAAA 512

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AR275665  
LOCUS AR275665 528 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 1 from patent US 6509172.  
ACCESSION AR275665  
VERSION AR275665.1 GI:29709167  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 528)  
AUTHORS De Bakker, O., Van den Eynde, B., and Boon-Falleur, T.  
TITLE Isolated, truncated nucleic acid which are members of the gage, and  
uses thereof  
JOURNAL Patent: US 6509172-A 1 21-JAN-2003;  
FEATURES Location/Qualifiers  
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Best Local Similarity 98.3%; Pred. No. 2.2e-120;  
Matches 521; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

QY 3 CTGTGAGGACGCTCTGTGTGTTCTCTGCGGTCCGAGTCTTTTCTCTACTGAGATCA 62  
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QY 63 TCTGTGTGAAATATGAGTTGGCGAGGAAGATCCACCTATTATTGGCCTAGACCAAGCGC 122  
Db 61 TCTGTGTGAAATATGAGTTGGCGAGGAAGATCCACCTATTATTGGCCTAGACCAAGCGC 117

QY 123 TATGTACAGCCTCTCTGAAGTGAATGGGCTTATGCGGCCGAGCAGTTTCACTGATGAAGTG 182  
Db 118 TACGTAGAGCCTCTCTGAATGAATGGGCTTATGCGGCCGAGCAGTTTCACTGATGAAGTG 177

QY 183 GATCCAGCAACACTGAGAGAGGGGACAGCAACTCAACGTCAGGATCTCGAGCTGCT 242  
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QY 243 CAGGAGGAGGAGGATGAGGAGGATCTGCAAGGTCAAGGGCCGAAGCCTGAAGCTGATAGC 302  
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QY 303 CAGGAACAGGCTTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGGAGGAG 362  
Db 298 CAGGAACAGGCTTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGGAGGAG 357

QY 363 ATGAGCCCGCAATCCAGAGAGGTTGAAAACCCCTGAAGAGGTGAAGAGCAATCACAG 422  
Db 358 ATGAGCCCGCAATCCAGAGAGGTTGAAAACCCCTGAAGAGGTGAAGAGCAATCACAG 417

QY 423 TGTTAAAGAAAGCAGCTTGAATATGATGAGGCTGCTCTATGTTGAAAATTTGTTCAAT 482  
Db 418 TGTTAAAGAAAGCAGCTTGAATATGATGAGGCTGCTCTATGTTGAAAATTTGTTCAAT 477

QY 483 AAAATTTCTCCCAATAAGCTTTTACAGCTTTCTGCAAGAAAAA 532  
Db 478 AAAATTTCTCCCAATAAGCTTTTACAGCTTTCTGCAAGAAAAA 527

RESULT 13  
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LOCUS AF055473 528 bp mRNA linear PRI 01-MAY-2000  
DEFINITION Homo sapiens GAGE-8 mRNA, complete cds.



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QY      481 TTAATAATTCCTCCAAATAAAGCTTTACAGCCTTCTGCAAAAGAAA 524
Db      487 TTAATAATTCCTCCAAATAAAGCTTTACAGCCTTCTGCAAAAGAAA 530

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LOCUS      AX886264      430 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 2127 from Patent EP1033401.
ACCESSION AX886264
VERSION    AX886264.1 GI:40043251
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE      Expressed sequence tags and encoded human proteins
JOURNAL    Patent: EP 1033401-A 2127 06-SEP-2000;
Genset (FR)

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Best Local Similarity 97.6%; Pred. No. 2e-80;
Matches 360; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

QY      1 AGCTGTAGGACAGTGTGTGTTCTCGCGTCCGGACTCTTTTCTCTACTGAGATT 60
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Db      123 CATCTGTGTAATATGAGTTGGCGAGAGATCGACTATTATTGGCCTAGACCAAGRC 181
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QY      241 CTCAGGAGGAGAGGATGAGGAGCATCTCAGGTCAAGGCCGCAAGCCTGAAGCTGATA 300
Db      302 CTCAGRAGGAGAGGATGAGGAGCATCTCAGGTCAAGGCCGCAAGCCTGAAGCTCATA 361
QY      301 GCCAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTTGATGGGCAGG 360
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QY      361 AGATGGACC 369
Db      422 AGATGGAMC 430
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-782-745-17

Perfect score: 532  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	512.8	96.4	527	12	BI826605
2	510.4	95.9	521	13	BX108227
3	506.6	95.2	517	14	CF780547
4	490.2	92.1	509	12	BI868671

C	5	476.4	89.5	489	9	AA447559	AA447559 zw81ell.s
C	6	452.2	85.0	457	10	AW510753	AW510753 hd39d05.x
C	7	443.6	83.4	464	9	AA738037	AA738037 nx15ell.s
C	8	442.2	83.1	447	9	AI381509	AI381509 te76b07.x
C	9	438.6	82.4	480	12	BG120336	BG120336 602353732
C	10	436	82.0	505	14	CB115693	CB115693 K-EST0159
C	11	431.6	81.1	450	9	AA760996	AA760996 nx32h08.s
C	12	417	78.4	455	9	AI187350	AI187350 gf29a05.x
C	13	407.4	76.6	418	9	AW016546	AW016546 UI-H-BIOP
C	14	398.8	75.0	426	9	AA688226	AA688226 ak48a07.s
C	15	377.8	71.0	383	12	BM836228	BM836228 K-EST0111
C	16	372.8	70.1	419	9	AA448542	AA448542 zw81ell.r
C	17	369	69.4	445	11	BC005363	BC005363 Homo sapi
C	18	360.6	67.8	412	9	AW102587	AW102587 xd67g07.x
C	19	334.4	62.9	384	9	AA913206	AA913206 om53f03.s
C	20	331	62.2	383	13	EX283580	EX283580 BX283580
C	21	318.8	59.9	397	12	BG206349	BG206349 RST25797
C	22	314.8	59.2	341	12	BP431265	BP431265 BP431265
C	23	314	59.0	398	9	AA918604	AA918604 ol53f02.s
C	24	307.2	57.7	333	13	BU533718	BU533718 AGENCOURT
C	25	300.8	56.5	320	12	BM836021	BM836021 K-EST0111
C	26	273.6	51.4	457	14	CF780497	CF780497 AGENCOURT
C	27	269.8	50.7	275	14	CB147043	CB147043 K-EST0202
C	28	269.8	50.7	275	14	CB150355	CB150355 K-EST0207
C	29	269.8	50.7	275	14	CB157288	CB157288 K-EST0216
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C	31	231.8	43.6	258	12	EG186708	EG186708 RST5683 A
C	32	226.6	42.6	253	12	EG184057	EG184057 RST2973 A
C	33	223.4	42.0	261	12	EG199060	EG199060 RST18336
C	34	221.6	41.7	245	12	BG212621	BG212621 RST32217
C	35	216.6	40.7	292	12	BG212622	BG212622 RST32217
C	36	213.2	40.1	245	12	BG208433	BG208433 RST27934
C	37	207.6	39.0	507	9	AA972716	AA972716 OP90e12.s
C	38	206.4	38.8	224	9	AA738394	AA738394 nx28cl2.s
C	39	205.4	38.6	256	12	BG216461	BG216461 RST36040
C	40	205.2	38.6	524	11	AF318372	AF318372 Homo sapi
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C	42	195.4	36.7	197	9	AI968311	AI968311 wu01f07.x
C	43	192.8	36.2	226	12	BG220441	BG220441 RST40225
C	44	192.4	36.2	499	12	BG354572	BG354572 PLAC6 Hum
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#### ALIGNMENTS

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DEFINITION 603077056F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5168892 5',
mRNA sequence.
ACCESSION BI826605
VERSION BI826605.1 GI:15938155
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 527)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11419 row: p column: 13
High quality sequence stop: 519.
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FEATURES
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Location/Qualifiers
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/clone="IMAGE:5168892"
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/site="Organ; brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dr primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC library."

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## ORIGIN

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QY	63	TCGTGTGAAATGATGTGGCGAGGAGATGCACCTATTATTGGCTACACCAAGCGC	122		
Db	61	TCGTGTGAAATGATGTGGCGAGGAGATGCACCTATTATTGGCTACACCAAGCGC	120		

123	TATGTACAGCCTCCTGAAGCTGATTGGGCCCTATCGGCCCGAGCAGTTCAGTGAAGTG	182
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121	TATGTACAGCCTCCTGAAGCTGATTGGGCCCTATCGGCCCGAGCAGTTCAGTGAAGTG	180
DB		
183	GAAACAGCAACCTCTGAAGAGGGGAACGAGCAACTCAAGTCAGGATCTTCAGAGTGCT	242
QY		
181	GAAACAGCAACCTCTGAAGAGGGGAACGAGCAACTCAAGTCAGGATCTTCAGAGTGCT	240
DB		

243	CHAGAGGGAGAGATAGCGGAGATCTCAGGTC	CAAGGCCGAGGCTGAAGCTGATAGC	302
	DB		
241	CAGGAGGGAGAGATAGCGGAGATCTCAGGTC	CAAGGCCGAGGCTGAAGCTCATAGC	300
303	CAGGAACGGGTCACCCACAGACTGGGTCGAGTGTGAAGATCGTCTCTGATGGCCAGGAG	362	
	QY		
301	CAGGAACAGGGTCACCCACAGACTGGGTCGAGTGTGAAGATCGTCTCTGATGGCCAGGAG	360	
	DB		

363 ATGAGCCCGCCAAATCCAGAGAGGTGAAACGCCCTGAAGAAGGTGAAAGCAATCACAG 422  
361 ATGAGCCCGCCAAATCCAGAGAGGTGAAACGCCCTGAAGAAGGTGAAAGCAATCACAG 420  
423 TGTAAAAAGAGGCACGTTGAAATGATGACAGGCTGCTCCTATGTTCGAAATTGTTCAAT 482  
421 TGTAAAAAGAGGCACGTTGAAATGATGACAGGCTGCTCCTATGTTCGAAATTGTTCAAT 480

```

QY      483   AAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA 530
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DbB     481   AAAATTCTCCCAATAAAGCTTTACAG-CTTCTGCAAGAAAAA 527

```

LOCUS  
DEFINITION  
IMAGE1.1256204, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BX1083227 521 bp mRNA linear EST 06-FEB-2003  
BX1083227 NCI CGAP GC3 Homo sapiens cDNA clone IMAGEp998K213161 ;  
BX1083227  
BX1083227.1 GI:27835080  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE AUTHORS	TITLE JOURNAL COMMENT
1. J. H. ...	...
2. J. H. ...	...
3. J. H. ...	...
4. J. H. ...	...
5. J. H. ...	...
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97. J. H. ...	...
98. J. H. ...	...
99. J. H. ...	...
100. J. H. ...	...

1 (bases 1 to 521)

Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,  
Radelof, U., Schneider, D. and Korn, B.

Human Unigeneset - RZPD3

JOURNAL  
COMMENT

RPZD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RPZD: IMAGO998K213161

RZPDLIB: I.M.-A.G.E.

Human UnigenesSet - RZPD3 (RZPDLIB No.972)

<http://www.rzpu.de/CloneCards/cgi-bin/showLib.cgi/regions2Libnc>

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101

Fax: +49 30 32639 111  
www.vand.d

This clone is available royalty-free from BZPD:

contact RZPD (clone@rzd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAACAGCTATGAC.

<b>FEATURES</b>	<b>SOURCE</b>
-----------------	---------------

/organism="Homo sapiens"

/mol\_type="mRNA"

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/db_xref="taxon:"  
/clone="TMAC00000"
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/tissue type="pooled germ cell tumors"

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/lab_host="DH10B"
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/note="Vector: nT"
```

polylinker; 1st strand cD

germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pVT73 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

## ORIGIN

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Query Match      95.9%; Score 510.4; DB 13; Length 521;
Best Local Similarity 98.8%; Pred. No. 5.8e-104;
Matches 514; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Qy	11	CAGTCTGTGTGGTTCCTCGGTCGGGACTCTTTTTCCTCTACTCAGATTCATCTGTGTG	70
Db	1	CAGTCTGTGTGGTTCCTCGGTCGGGACTCTTTTTCCTCTACTCAGATTCATCTGTGTG	60

QY	71	AAATATGAGTTGGCAGGAGAGATCGACCTATTATTGGCCCTAGACCAAGGCGCTATGACA	130
D6	61 <th>AAATATGAGTTGGCAGGAGAGATCGACCTATTATTGGCCCTAGTCGAGAGCGCTATGTCG</th> <th>120</th>	AAATATGAGTTGGCAGGAGAGATCGACCTATTATTGGCCCTAGTCGAGAGCGCTATGTCG	120

QY		GCCTCCTGAAGTGATTGGGCGCTATCCGGGCCCGAGCAGTTCAGTAGTGATGAAGTGGAACCAAGC	190
D6		GCTTCTCTGTAAATGTTTCCGACTATATGACCGCATCGTCTCTGATCTCTAATTAATCTCTATTTT	200

191 AACCTGAAGAGGGGAACGACAACTCAACGTCAGGATCTCGAGCTGCTCAGGAGG 250

251 AGAGGATGAGGGAGGACATCTGCAGGTCAAGGCCGAGCCTGAAGCTGATAGCCGAGAACA 310

311 GGGTCAACCCACAGACTGGTGTGAGTGTGAAGATGGTCTCTGATGGGCAGAGATGGACCC 370

371 GCCTAAATCCAGAGAGGTGAAACCCCTGAAGAGGTGAAAAGCAATCAAGTGTAAAA 430

431 GAAGGCAGCTTGAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTTCATATAAATTCT 490



```

Db      421 GAAGGACAGTTGAATGATGAGGCTCTCTATGTTGGAATTTGTTCAATAAATCT 480
|||||
QY      491 CCCAATAAAGCTTTACAGCTTTCTGCAAAAGAAAAA 530
|||||
Db      481 CCCAATAAAGCTTTACAGCTTTCTGCAAAAGAAAAA 520
|||||

RESULT 3
CF780547      517 bp mRNA linear EST 20-OCT-2003
AGENCY: 1579102 NIH MGC 217 Homo sapiens cDNA clone
IMAGE: 30524555 5', mRNA sequence.
ACCESSION    CF780547
VERSION      CF780547.1 GI:37739989
KEYWORDS     EST.
SOURCE       Homo sapiens
ORGANISM     Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 517)
AUTHORS      NIH-MGC http://mgi.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Daniela S. Gerhard, Ph.D.
              Office of Cancer Genomics
              National Cancer Institute / NIH
              Bldg. 31 Rm10A07 Bethesda, MD 20892
              Email: cgaabs@mail.nih.gov
              Tissue Procurement: James Martin, University of Iowa
              cDNA Library Preparation: M. Bento Soares, University of Iowa
              DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
              Clone distribution by: Agencourt Bioscience Corporation
              found through the MGC clone distribution information can be
              http://image.llnl.gov
              Plate: NDAM604 row: e column: 12
              High quality sequence stop: 517.
FEATURES     source
              1..517
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:30524555"
                /cisse_type="pooled Chondrosarcoma Tumor cells"
                /lab_host="NIH MGC 217"
                /clone_lib="NIH MGC 217"
                /notes="Vector: pYX-Asc; Site 1: EcoRI; Site 2: NotI;
                Library is oligo-dT primed and directionally cloned.
                Denatured RNA was size fractionated on a 1% agarose gel.
                primer containing a Not I site. Double strand cDNA was
                size selected according to mRNA size fraction, ligated with
                EcoR I adaptor, digested with Not I and then cloned
                directionally into pYX-Asc vector. Average insert size
                0.5-1kb. Adaptors 5' (AATTGGCAGCAGG)3' and 5'd
                (CTCTGCGG)3'. 3' linker sequence - GGGCGCTGAGAGCC T18.
                Sequencing primers 3' end: T3 promoter primer 5'd
                (ATTAACTCTCACTAAGGA)3'. 5' End: T7 promoter primer 5'd
                (TAATACGACTCACTATAGG)3'. Average insert size 0.5-1kb.
                Library was constructed in the laboratory of M. Bento
                Soares. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 95.2%; Score 506.6; DB 14; Length 517;
Best Local Similarity 99.2%; Pred. No. 4.1e-103;
Matches 509; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      5 GTGAGGAGTGTGTGTGTTCTGCGCTCGGACTTTTCTCTACTGAGATTCATC 64
|||||
Db      4 GAGGGGAGTGTGTGTGTTCTGCGCTCGGACTTTTCTCTACTGAGATTCATC 63
|||||
QY      65 TGTGTGAATATGAGTTGGCGAGGAGATCGACCTATTATTGGCTTACCAAGGGCTA 124
|||||

```

```

Db      64 TGTGTGAATATGAGTTGGCGAGGAGATCGACCTATTATTGGCTTACCAAGGGCTA 123
|||||
QY      125 TGTACAGCTCTCTGAAGTGATTGGGCTTATGCGGCCGAGAGCTTCAGTGTGAAGTGA 184
|||||
Db      124 TGTACAGCTCTCTGAAGTGATTGGGCTTATGCGGCCGAGAGCTTCAGTGTGAAGTGA 183
|||||
QY      185 ACCAGCAACACTCTGAAGAGGGGACCACTCAAGCTCAGGATCCTGCGAGCTGCTCA 244
|||||
Db      184 ACCAGCAACACTCTGAAGAGGGGACCACTCAAGCTCAGGATCCTGCGAGCTGCTCA 243
|||||
QY      245 GGAGGAGAGGATGAGGAGCATCTGCAGGTCAGAGGCCGAGAGCTTGAAGCTCATAGCCA 304
|||||
Db      244 GGAGGAGAGGATGAGGAGCATCTGCAGGTCAGAGGCCGAGAGCTTGAAGCTCATAGCCA 303
|||||
QY      305 GGAAACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGTGTCTCTGATGGGAGAGAT 364
|||||
Db      304 GGAAACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGTGTCTCTGATGGGAGAGAT 363
|||||
QY      365 GGACCCGCCAATCCAGAGGAGTGAACCGCTGAAGAGCTGAAAGCAATCACAGTG 424
|||||
Db      364 GGACCCGCCAATCCAGAGGAGTGAACCGCTGAAGAGCTGAAAGCAATCACAGTG 423
|||||
QY      425 TTAAAAGAGGCACCGTTGAAATGATCGAGCTGCTCTATGTTGAAAATTTCTTCATTAA 484
|||||
Db      424 TTAAAAGAGGCACCGTTGAAATGATCGAGCTGCTCTATGTTGAAAATTTCTTCATTAA 483
|||||
QY      485 AATTCTCCCAATAAAGCTTTTACAGCTTCTGCA 517
|||||
Db      484 AATTCTCCCAATAAAGCTTTTACAGCTTCTGCA 516
|||||

RESULT 4
BI868671      509 bp mRNA linear EST 11-OCT-2001
LOCUS        603392594F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5402663 5',
              mRNA sequence.
ACCESSION    BI868671
SOURCE       Homo sapiens
ORGANISM     Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 509)
AUTHORS      NIH-MGC http://mgi.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgaabs@mail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM12026 row: 1 column: 24
              High quality sequence stop: 509.
FEATURES     source
              1..509
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:5402663"
                /cisse_type="adenocarcinoma, cell line"
                /lab_host="PH10B (phage-resistant)"
                /clone_lib="NIH_MGC_90"
                /note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
                Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
                Average insert size 1.7 kb. Library enriched for
                full-length clones and constructed by Life Technologies.
                Note: this is a NIH_MGC Library."

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ORIGIN		FEATURES		Location/Qualifiers	
Query Match		source		1. 489	
Best Local Similarity				/organism="Homo sapiens"	
Matches 492; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				/mol_type="mrna"	
				/db_xref="taxon:9606"	
				/clone="IMAGE:782636"	
				/sex="male"	
				/lab_host="DH10B"	
				/clone_lib="Soares testis_NHT"	
				/note="vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5]"	
				TGTTACCAATCTGAAGTGGGAGCGGCCCAATTTTTTTTTTTT 34]	
				Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went through one round of normalization to Cots, and was constructed by Bento Soares and M. Fatima Bonaldo."	
ORIGIN		Query Match		89.5%; Score 476.4; DB 9; Length 489;	
		Best Local Similarity		99.6%; Pred. No. 2.4e-96;	
		Matches 488; Conservative 0; Mismatches 1; Indels 1; Gaps 1;			
Qy	34	CCGGACCTTTTTCCTCTACTGAGATTCATCTGTGTAATATGAGTTGGCGAGAGAT	93		
Db	489	CCGGACCTTTTTCCTCTACTGAGATTCATCTGTGTAATATGAGTTGGCGAGAGAT	430		
Qy	94	CGACCTATTATTGGCCCTAGACCAAGGCGCTATGTATACAGCCTCTTGAAGTGAATTCGGGCTTA	153		
Db	429	CGACCTATTATTGGCCCTAGACCAAGGCGCTATGTATACAGCCTCTTGAAGTGAATTCGGGCTTA	371		
Qy	154	TGGGCCCCGAGCAGTTTCAGTGATGAAGTGAAGCCAGCAACCTTGAAGAGGGGAAACGAG	213		
Db	370	TGGGCCCCGAGCAGTTTCAGTGATGAAGTGAAGCCAGCAACCTTGAAGAGGGGAAACGAG	311		
Qy	214	CAACTCAACCTCAGGATCTCTGAGGAGGAGGAGGATGAGGGAGCATCTGCAG	273		
Db	310	CAACTCAACCTCAGGATCTCTGAGGAGGAGGAGGATGAGGGAGCATCTGCAG	251		
Qy	274	GTCAAGGGCCGAAAGCCTGAAGCTGATAGCCAGGAACAGGGGTCAACCCACAGACTGGGTGTG	333		
Db	250	GTCAAGGGCCGAAAGCCTGAAGCTGATAGCCAGGAACAGGGGTCAACCCACAGACTGGGTGTG	191		
Qy	334	AGTGTGAAGATGTCTTGATGGCGAGAGATGAGCCGCCAAATCCAGAGAGGTGAAA	393		
Db	190	AGTGTGAAGATGTCTTGATGGCGAGAGATGAGCCGCCAAATCCAGAGAGGTGAAA	131		
Qy	394	CGCTCTGAAGAGGTGAAGCAATCAAGTGTAAAGAGGAGGACGTTGAAATGATGCAG	453		
Db	130	CGCTCTGAAGAGGTGAAGCAATCAAGTGTAAAGAGGAGGACGTTGAAATGATGCAG	71		
Qy	454	GCTGCTCTTATGTTGAAATTTGTCATTAATAATTTCTCCCAATAAAGCTTTTACAGCCTTC	513		
Db	70	GCTGCTCTTATGTTGAAATTTGTCATTAATAATTTCTCCCAATAAAGCTTTTACAGCCTTC	11		
Qy	514	TGCAAGAGAA	523		
Db	10	TGCAAGAGAA	1		
RESULT 6		AW510753/c		457 bp	
LOCUS		AW510753		mRNA	
DEFINITION		hd39d05.x1 Soares_NFL T_GBC S1 Homo sapiens cDNA clone		linear	
		IMAGE:2911881 3', similar to SW:GGE4_HUMAN Q13068 GAGE-4 PROTEIN. ;		EST 03-MAR-2000	
		mRNA sequence.			
ACCESSION		AW510753			
VERSION		AW510753.1		GI:7148831	
KEYWORDS		EST.			
SOURCE		Homo sapiens (human)			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 489)		Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, J., Wyllie, J., Waterston, R. and Wilson, R.		WashU-Merck EST Project 1997	
Unpublished (1997)		Contact: Wilson RK		Washington University School of Medicine	
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108		Tel: 314 286 1800		Fax: 314 286 1810	
Email: est@wustl.edu		This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.		Seq primer: -4ml3 fwd. Ef from Amersham	
High quality sequence stop: 427.					

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 457)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
FEATURES
source
1..457
/organism="Homo sapiens"
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/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not 1; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
ORIGIN
Query Match 85.0%; Score 452.2; DB 10; Length 457;
Best Local Similarity 99.3%; Pred. No. 6.3e-91;
Matches 454; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 68 GTGAATATGATGGCGAGGAGATCGACCTATTATTGGCTAGACCAAGCGCTATGT 127
Db |
457 GTGAATATGATGGCGAGGAGATCGACCTATTATTGGCTAGACCAAGCGCTATGT 398
QY 128 ACAGCTCTCTGAATGATGGGCTATGGCCGAGCGAGCTTCAGTGATGAGTGAAC 187
Db |
397 ACAGCTCTCTGAATGATGGGCTATGGCCGAGCGAGCTTCAGTGATGAGTGAAC 338
QY 188 AGCAACCTGTAAGAGGGGAACCGCAACTCAAGCTCAGGATCTCTGCAAGTCTCAGGA 247
Db |
337 AGCAACCTGTAAGAGGGGAACCGCAACTCAAGCTCAGGATCTCTGCAAGTCTCAGGA 278
QY 248 GGGAGAGGATGAGGAGCATCTGCAGGTCAGGGCCGAGCGGCAAGCTGAGCTGATGACGAGGA 307
Db |
277 GGGAGAGGATGAGGAGCATCTGCAGGTCAGGGCCGAGCGGCAAGCTGAGCTGATGACGAGGA 218
QY 308 ACAGGTCACCCACAGACTGGGTGTGAGTGTCAAGATGGTCTCTGATGGCGAGGATGGA 367
Db |
217 ACAGGTCACCCACAGACTGGGTGTGAGTGTCAAGATGGTCTCTGATGGCGAGGATGGA 158
QY 368 CCCGCAATTCAGAGGAGGTGAAACCGCTGAAGAAGGTGAAAGCAATCACAGTGTTA 427
Db |
157 CCCGCAATTCAGAGGAGGTGAAACCGCTGAAGAAGGTGAAAGCAATCACAGTGTTA 98
QY 428 AAAGAAGGCACGCTGAATGATGACGAGTGTCTTATGTTGAAATTTGTTCAATTAAT 487
Db |
97 AAAGAAGGCACGCTGAATGATGACGAGTGTCTTATGTTGAAATTTGTTCAATTAAT 38
QY 488 TCTCCCAATAAGCTTTTACAGCTTCTGCAAGAAAA 524
Db |
37 TCTCCCAATAAGCTTTTACAGCTTCTGCAAGAAAA 1
RESULT 7

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```

AA738037/c
LOCUS AA738037 464 bp mRNA linear EST 22-JAN-1998
DEFINITION rx15e11.s1 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1256204 3',
similar to TR:Q13070 Q13070 GAGE-6 PROTEIN.; mRNA sequence.
ACCESSION AA738037
VERSION AA738037.1 GI:2768794
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 464)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert length: 511 Std Error: 0.00
Seq primer: -40md3 fwd. ET from Amersham
High quality sequence stop: 435.
FEATURES
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/db_xref="taxon:9606"
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/tissue_type="pooled germ cell tumors"
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/clone_lib="NCI CGAP GC3"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is not normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."
ORIGIN
Query Match 83.4%; Score 443.6; DB 9; Length 464;
Best Local Similarity 98.0%; Pred. No. 5.3e-89;
Matches 449; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 75 ATGAGTTGGCGAGGAGATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCT 134
Db |
464 ATGAGTTGGCGAGGAGATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCT 405
QY 135 CCTGAAGTGTATGGCCCTATCGGCCGAGCAGTTTCAGTGATGAGTGAACCAACA 194
Db |
404 CTGAAATGATTTGGCCCTATGCAGCCGAGCAGTTTCAGTGATGAGTGAACCAACA 345
QY 195 CTGAAGAGGGGACACAGCAACTCAAGCTCAGGATCTCTGAGTGTCTGAGGAGGAG 254
Db |
344 CTGAAGAGGGGACACAGCAACTCAAGCTCAGGATCTCTGAGTGTCTGAGGAGGAG 285
QY 255 GATGAGGAGGATCTGCAAGGTCAGGGCCGAGGCTGAAGCTGTAGCCAGGAACAGG 314
Db |
284 GATGAGGAGGATCTGCAAGGTCAGGGCCGAGGCTGAAGCTGTAGCCAGGAACAGG 225
QY 315 CACCCACAGCTGGGTGTGAGTGTGAGATGGTCTGATGGCGAGGATGACCCGCCA 374
Db |
224 CACCCACAGCTGGGTGTGAGTGTGAGATGGTCTGATGGCGAGGATGACCCGCCA 165
QY 375 AATCAGAGGAGGTGAAAAACCCCTGAAGAGGTGAAAAAGCAATCACAGTGTAAAAAG 434

```

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Db      164 ATCCAGAGAGGTGAACGCTTGAGAGGTGGAAGCAATCACAGTGTATAAGAGAG 105
QY      435 GCACGTTGAATGATGACGCTGCTCTATGTTGGAAAATTGTTCAATAAATCTCCCA 494
Db      104 GCACGTTGAATGATGACGCTGCTCTATGTTGGAAAATTGTTCAATAAATCTCCCA 45
QY      495 ATAAAGCTTTACAGCTTCTGCAAGAAAATAAAAAAAA 532
Db      44 ATAAGAGTTTACAGCTTCTGCAAAAAATAAAAAAAA 7

RESULT 8
AI381509/c
LOCUS   AI381509                447 bp    mRNA    linear    EST 28-MAR-1999
DEFINITION te76507.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2092597 3' similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;, mRNA sequence.
ACCESSION AI381509
VERSION   AI381509.1 GI:4194290
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 447)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
          Insert Length: 497 Std Error: 0.00
          Seq primer: -40Up from Gibco.

FEATURES             source
     source          1..447
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:2092597"
                    /lab_host="DH10B"
                    /clone_lib="Soares_NFL_T_QBC_S1"
                    /note="Organ: pooled; Vector: pTZ19-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCI CGAP GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match      83.1%; Score 442.2; DB 9; Length 447;
Best Local Similarity 99.3%; Pred. No. 1.1e-88;
Matches 444; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      79 GTTCGCGAGGAGATCGACCTATTATTCGCTAGACCAAGCGCTATGACAGCTCTCTG 138
Db      447 GTTCGCGAGGAGATCGACCTATTATTCGCTAGACCAAGCGCTATGACAGCTCTCTG 388
QY      139 AAGTGATTTGGGCTATCGGGCCGAGCGAGTTTCAGTGATGAAGTGAACCAACACCTG 198
Db      387 AATGATTTGGGCTATCGGGCCGAGCGAGTTTCAGTGATGAAGTGAACCAACACCTG 328
QY      199 AAGAAGGGGAACCAACCACTCAACGTCAGGATCTTCGAGCTCTCAGGAGGAGGATG 258
Db      327 AAGAAGGGGAACCAACCACTCAACGTCAGGATCTTCGAGCTCTCAGGAGGAGGATG 268

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QY      259 AGGGAGCATCTGCAGGTCAAGGCCGAGCCTGAAGCTGATAGCCAGGAACAGGGTCACC 318
Db      267 AGGGAGCATCTGCAGGTCAAGGCCGAGCCTGAAGCTGATAGCCAGGAACAGGGTCACC 208
QY      319 CACAGACTGGGTGTGAGTGTGAAGATGTCCTCATGCGCAGGAGATGGACCCGCAATC 378
Db      207 CACAGACTGGGTGTGAGTGTGAAGATGTCCTCATGCGCAGGAGATGGACCCGCAATC 148
QY      379 CAGAGGAGGTGAAAACGCTTGAAGAAGCAATCACAGTGTGTAAGAAAGAGGCAC 438
Db      147 CAGAGGAGGTGAAAACGCTTGAAGAAGCAATCACAGTGTGTAAGAAAGAGGCAC 88
QY      439 GTTGAATGATGACGAGCTGCTCTATGTTGGAAAATTGTTCAATAAATCTCCCAATAA 498
Db      87 GTTGAATGATGACGAGCTGCTCTATGTTGGAAAATTGTTCAATAAATCTCCCAATAA 28
QY      499 AGCTTTACAGCTTCTGCAAGAAAAA 525
Db      27 AGCTTTACAGCTTCTGCAAGAAAAA 1

RESULT 9
BG120336
LOCUS   BG120336                480 bp    mRNA    linear    EST 30-JAN-2001
DEFINITION 602353732F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4451958 5', mRNA sequence.
ACCESSION BG120336
VERSION   BG120336.1 GI:12613845
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 480)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LHAM10239 row: p column: 07
          High quality sequence stop: 480.

FEATURES             source
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                    /db_xref="taxon:9606"
                    /clone="IMAGE:4451958"
                    /tissue_type="adenocarcinoma, cell line"
                    /lab_host="DH10B (phage-resistant)"
                    /clone_lib="NIH_MGC_90"
                    /note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 Kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN
Query Match      82.4%; Score 438.6; DB 12; Length 480;
Best Local Similarity 99.1%; Pred. No. 7e-88;
Matches 441; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      88 GAAGATCGACCTATTATTCGCTAGACCAAGCGCTATGATACAGCTCTCTGAAGTGATG 147
Db      1 GAAGATCGACCTATTATTCGCTAGACCAAGCGCTATGATACAGCTCTCTGAAGTGATG 60

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QY 148 GGCTATGCGGCCGAGCGAGTTCAGTGATGAAGTGGAACACAGCAACACCTGAGAGGGG 207  
DB 61 GGCTATGCGGCCGAGCGAGTTCAGTGATGAAGTGGAACACAGCAACACCTGAGAGGGG 120  
QY 208 AACACCAACTCAACGTCAGGATCCTGACGCTGCTCAGGAGGAGAGGATGAGGAGCAT 267  
DB 121 AACACCAACTCAACGTCAGGATCCTGACGCTGCTCAGGAGGAGAGGATGAGGAGCAT 180  
QY 268 CTGCAAGTCAAGGCGGAGACCTGAGCTGATGATGATGATGATGATGATGATGATGATG 327  
DB 181 CTGCAAGTCAAGGCGGAGACCTGAGCTGATGATGATGATGATGATGATGATGATGATG 240  
QY 328 GGTGTCAGTGTCAAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 387  
DB 241 GGTGTCAGTGTCAAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 300  
QY 388 TGAACACGCTCAAGAGGATGAAAGCAATCAAGTGTGTTAAAGAGGACACCTGTTAAATG 447  
DB 301 TGAACACGCTCAAGAGGATGAAAGCAATCAAGTGTGTTAAAGAGGACACCTGTTAAATG 360  
QY 448 ATGCAAGTCTCCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 507  
DB 361 ATGCAAGTCTCCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 420  
QY 508 GCCTTCTGCAAAAGAAAAA 532  
DB 421 GCCTTCTGCAAAAGAAAAA 445

RESULT 10  
LOCUS CB115693  
DEFINITION K-EST0159805 L8SCK0 Homo sapiens cDNA clone L8SCK0-8-B09 5', mRNA  
sequence.  
ACCESSION CB115693  
VERSION CB115693.1 GI:27941500  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 505)  
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
Kim,Y.S.  
TITILE 21C Frontier Korean EST Project 2001  
JOURNAL Unpublished (2002)  
COMMENT Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 8 row: B column: 09  
High quality sequence stop: 505.  
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Location/Qualifiers  
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/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="L8SCK0-8-B09"  
/sex="M"  
/cell\_line="SCK"  
/lab\_host="Top10F"  
/clone\_lib="L8SCK0"  
/note="Organ: Liver; Vector: pVT3-Pac; Site 1: EcoRI;  
Site 2: NotI; The library was contributed by the Soares  
laboratory and it was constructed as described by Bonaldo,  
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research  
6(9): 791-806. RNA was prepared from harvested cell  
culture."

Query Match 82.0%; Score 436; DB 14; Length 505;  
Best Local Similarity 97.8%; Pred. No. 2.7e-87;  
Matches 442; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
QY 23 GTTCTGCGGTCGAGCTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 82  
DB 19 GGTCTGCGGTCGAGCTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 78  
QY 83 GCGAGGAATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCTCTCTCAAGT 142  
DB 79 GCGAGGAATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCTCTCTCAAT 138  
QY 143 GATTGGGCTTATGCGGCGGAGCAGTTCAGTGTGATGATGATGATGATGATGATGATGATG 202  
DB 139 GATTGGGCTTATGCGGCGGAGCAGTTCAGTGTGATGATGATGATGATGATGATGATGATG 198  
QY 203 AGGGGAACCAAGCAACTCAACGTCAGGATCCTGACGCTGCTCAGGAGGAGAGATGAGGG 262  
DB 199 AGGGGAACCAAGCAACTCAACGTCAGGATCCTGACGCTGCTCAGGAGGAGAGATGAGGG 258  
QY 263 AGCATCTGAGGTCAAGGCGGCAAGCCTGAAGCTGATAGCCAGGAACAGGGGTCAACCACA 322  
DB 259 AGCATCTGAGGTCAAGGCGGCAAGCCTGAAGCTGATAGCCAGGAACAGGGGTCAACCACA 318  
QY 323 GACTGGGTGTGATGTGAAGATGCTCTGATGGGAGGAGATGAGCCGCAAAATCCAGA 382  
DB 319 GACTGGGTGTGATGTGAAGATGCTCTGATGGGAGGAGATGAGCCGCAAAATCCAGA 378  
QY 383 GGAGGTGAAGAGCGCTGAGGAGGTGAAGCAATCAGTGTGTTAAAGAGGACGCTTG 442  
DB 379 GGAGGTGAAGAGCGCTGAGGAGGTGAAGCAATCAGTGTGTTAAAGAGGACATGCTG 438  
QY 443 AAATGATGAGGCTGCT 474  
DB 439 AAATGATGAGGCTGCT 470

RESULT 11  
LOCUS AA760996  
DEFINITION nx32h08.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1257855 3'  
similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. i, mRNA sequence.  
ACCESSION AA760996  
VERSION AA760996.1 GI:2809926  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 450)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITILE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 331.  
FEATURES  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:1257855"

/tissue type="pooled germ cell tumors"

/lab host="DH10B"

/clone lib="NCI CGAP GC4"

/note="Vector: p773D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

# ORIGIN

Query Match 81.1%; Score 431.6; DB 9; Length 450;  
Best Local Similarity 98.7%; Pred. No. 2.6e-86;  
Matches 445; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 75 ATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCCT 134  
Db 450 ATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCCT 391

QY 135 CCTGAAGTGATTGGGCTATCGCGCCGAGCGCTTCAGTGTGAAGTGGACAGCAACA 194  
Db 390 CCTGAAGTGATTGGGCTATCGCGCCGAGCGCTTCAGTGTGAAGTGGACAGCAACA 331

QY 195 CCTGAAGTGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCCT 254  
Db 330 CCTGAAGTGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCCT 271

QY 255 GATGAGGAGCATCTGCAGTCAAGGCCGAGCGCTGAAGCTGATGAGTGGACAGCAACA 314  
Db 270 GATGAGGAGCATCTGCAGTCAAGGCCGAGCGCTGAAGCTGATGAGTGGACAGCAACA 211

QY 315 CACCCAGACTGGTGTGAGTGTGAAGTGGTCTGATGGCGAGGAGTGGACCGCCCA 374  
Db 210 CACCCAGACTGGTGTGAGTGTGAAGTGGTCTGATGGCGAGGAGTGGACCGCCCA 151

QY 375 AATCCAGAGGAGTGAAGAGCGCTGAAAGAGGTGAAAGCAATCACAGTGTGTAAGAGAG 434  
Db 150 AATCCAGAGGAGTGAAGAGCGCTGAAAGAGGTGAAAGCAATCACAGTGTGTAAGAGAG 91

QY 435 GCAGTTGAAATGATGAGGCTGCTCTATGTTGGAAATTTGTTTCAATAAATCTCCCA 494  
Db 90 ACAGTTGAAATGATGAGGCTGCTCTATGTTGGAAATTTGTTTCAATAAATCTCCCA 31

QY 495 ATAAAGCTTTACAGCTTCTGCAAGAAAA 525  
Db 30 ATAAAG-TTTACAGCTTCTGCAAGAAAA 1

RESULT 12  
AI187350/c  
LOCUS  
DEFINITION  
qt29405.x1 Soares testis\_NHT Homo sapiens cDNA clone IMAGE:1751408  
3', similar to SW:GGE4\_HUMAN Q13068 GAGE-4 PROTEIN. [1] ; mRNA  
sequence.

ACCESSION  
AI187350  
VERSION  
AI187350.1 GI:3737988  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
REFERENCE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 455)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
AUTHORS  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL  
Unpublished (1997)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-re@mail.nih.gov  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert length: 504 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 391.

## FEATURES

source

1. .455  
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/clone="IMAGE:1751408"  
/sex="male"  
/lab\_host="DH10B"  
/clone\_lib="Soares testis\_NHT"  
/note="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5].  
Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 78.4%; Score 417; DB 9; Length 455;  
Best Local Similarity 97.4%; Pred. No. 4.8e-83;  
Matches 445; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

QY 75 ATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCCT 134  
Db 455 ATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCCT 398

QY 135 CCTGAAGTGATTGGGCTATCGCGCCGAGCGCTTCAGTGTGAAGTGGACAGCAACA 194  
Db 397 CCTGAAGTGATTGGGCTATCGCGCCGAGCGCTTCAGTGTGAAGTGGACAGCAACA 338

QY 195 CCTGAAGAGGGGAACAGCAACTCAACGTCAGGATCCTGAGTCTGAGGAGGAGAG 254  
Db 337 CCTGAAGAGGGGAACAGCAACTCAACGTCAGGATCCTGAGTCTGAGGAGGAGAG 278

QY 255 GATGAGGAGCATCTGCAGTCAAGGCCGAGCGCTGAAGCTGATGAGTGGACAGCAACA 314  
Db 277 GATGAGGAGCATCTGCAGTCAAGGCCGAGCGCTGAAGCTGATGAGTGGACAGCAACA 218

QY 315 CACCCAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGCGAGGAGTGGACCGCCA 374  
Db 217 CACCCAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGCGAGGAGTGGACCGCCA 158

QY 375 AATCCAGAGGAGTGAAGAGCGCTGAAGAGTGAAGAGCAATCACAGTGTGTAAGAGAG 434  
Db 157 AATCCAGAGGAGTGAAGAGCGCTGAAGAGTGAAGAGCAATCACAGTGTGTAAGAGAG 98

QY 435 GCAGTTGAAATGATGAGGCTGCTCTATGTTGGAAATTTGTTTCAATAAATCTCCCA 494  
Db 97 ACAGTTGAAATGATGAGGCTGCTCTATGTTGGAAATTTGTTTCAATAAATCTCCCA 38

QY 495 ATAAAGCTTTACAGCTTCTGCAAGAAAA 531  
Db 37 ATAAAGCTTTCCAGCTTCTGCAAGAAAA 1

## RESULT 13

AW016546/c  
LOCUS  
DEFINITION  
UT-H-BIOP-abg-g-06-0-UI.s1 NCI\_CGAP\_Sub2 Homo sapiens cDNA clone  
IMAGE:271196 3', mRNA sequence.  
ACCESSION  
AW016546  
VERSION  
AW016546.1 GI:5865303





Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "

## ORIGIN

```
Query Match          75.0%; Score 398.8; DB 9; Length 426;
Best Local Similarity 96.7%; Pred. No. 5.7e-79;
Matches 406; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 102 TATTGGCTAGACCAAGCGCTATGTACAGCTCTCTGAAAGTGAATGGGCTATGCGGCC 161
    |||
Db 420 TATCGGCTAGACCAAGCGCTAGAGCTCTCTGAAATGNANTTGCCTATGCGGCC 361
    |||

QY 162 GACAGTTCAGTGTAGTGAAGTGGACACAGCAACACCTTGAAAGGGGACAGCAACTCAA 221
    |||
Db 360 GACAGTTCAGTGTAGTGAAGTGGACACAGCAACACCTTGAAAGGGGACAGCAACTCAA 301
    |||

QY 222 CGTCAGGATCTGAGCTGCTCAGGGAGGAGAGGATGAGGAGCATCTGCAGGTCAAGGG 281
    |||
Db 300 CGTCAGGATCTGAGCTGCTCAGGGAGGAGAGGATGAGGAGCATCTGCAGGTCAAGGG 241
    |||

QY 282 CCGAAGCTGAAGTGTATAGCCAGGAACAGGGTCAACCAAGAGTGGTGTGTGTGAA 341
    |||
Db 240 CCGAAGCTGAAGTGTATAGCCAGGAACAGGGTCAACCAAGAGTGGTGTGTGTGAA 181
    |||

QY 342 GATGGTCTCATGGGAGGAGTGGACCCGCCAAATCCAGAGGAGTGAAGAGCGCTGAA 401
    |||
Db 180 GATGGTCTCATGGGAGGAGTGGACCCGCCAAATCCAGAGGAGTGAAGAGCGCTGAA 121
    |||

QY 402 GAAGGTGAAAGCAATCACAGTGTGTTAAAGAGGACAGCTTGAATGATGAGGCTGCTCC 461
    |||
Db 120 GAAGGTGAAAGCAATCACAGTGTGTTAAAGAGGACAGCTTGAATGATGAGGCTGCTCC 61
    |||

QY 462 TATGTTGGAATTTGTTCAATTAATTTCTCCCAATAAGCTTTACAGCTTTCGAAAGA 521
    |||
Db 60 TATGTTGGAATTTGTTCAATTAATTTCTCCCAATAAGCTTTACAGCTTTCGAAAGA 1
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## RESULT 15

BM836228  
LOCUS K-EST011762 S5SNU484s1 Homo sapiens cDNA clone S5SNU484s1-15-D07  
DEFINITION 5', mRNA sequence.

ACCESSION BM836228

VERSION BM836228.1 GI:19192637

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 383)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,

Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

Kim,Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 15 row: D column: 07

High quality sequence stop: 383.

Location/Qualifiers

1..383

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/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="S5SNU484s1-15-D07"

## FEATURES

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Search completed: August 6, 2004, 20:52:27

Job time : 2417 secs

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/lab\_host="Top10F"  
/clone lib="S5SNU484s1"  
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Site 2: NotI; The poly (A)+ RNA was decapped with tobacco  
acid pyrophosphatase (TAP) and ligated with DNA-RNA linker  
including EcoRI site by treatment of T4 RNA ligase. The  
first strand cDNA was synthesized from oligo dT-selected  
mRNA by priming with dT-tailed vector. The dT-tailed  
vector was adjusted to have about 60nt. The cDNA vector  
was circularized with E. coli DNA ligase after digestion  
of EcoRI which site is also included in vector. An RNA  
strand converted to a DNA strand by Okayama-Berg method.  
The obtained cDNA vectors were used for transformation of  
competent cells E. coli Top10F' by electroporation method.  
After analyzing and sequencing about 2,000 ~ 3,000  
colonies in original cDNA library, the abundant cDNAs were  
selected and amplified by PCR reaction using vector region  
primer including T7 promoter as 5' primer and N(dT)14 as  
3' primer. The PCR products were used as template for  
synthesis of biotinylated single stranded RNA by in vitro  
transcription reaction. The synthesized RNA probes were  
hybridized with antisense single stranded cDNAs prepared  
from original library and incubated with avidin-gel.  
After removing DNA-RNA hybrids by centrifuge, the  
subtracted cDNA libraries were constructed by  
transformation of the remaining DNA into competent cells E.  
coli Top10F' with electroporation method."

## ORIGIN

```
Query Match          71.0%; Score 377.8; DB 12; Length 383;
Best Local Similarity 99.5%; Pred. No. 2.9e-74;
Matches 379; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 62 ATCTGTGTGAATATGAGTTGGCGAGAGATCGACCTATTATTGGCCTAGACCAAGGCG 121
    |||
Db 3 ATCTGTGTGAATATGAGTTGGCGAGAGATCGACCTATTATTGGCCTAGACCAAGGCG 62
    |||

QY 122 CTATGTACAGCTCTCTGAGTGAATGGGCTATGCGGCCGAGCAGTTCAGTGAAGT 181
    |||
Db 63 CTATGTACAGCTCTCTGAGTGAATGGGCTATGCGGCCGAGCAGTTCAGTGAAGT 122
    |||

QY 182 GGAACAGCAACACCTGAAGAAGGGAAACAGCAACTCAACGTCAGGATCCTGCAGCTGC 241
    |||
Db 123 GGAACAGCAACACCTGAAGAAGGGAAACAGCAACTCAACGTCAGGATCCTGCAGCTGC 182
    |||

QY 242 TCAGGAGGGAGAGGATGAGGAGCATCTGCAGTCAAGGCCGAGCCTGAAGCTGTAG 301
    |||
Db 183 TCAGGAGGGAGAGGATGAGGAGCATCTGCAGTCAAGGCCGAGCCTGAAGCTGTAG 242
    |||

QY 302 CCGAGAACAGGTCACCCACAGACTGGTGTGAGTGAAGAGTGTCTCTGATGGCGAGGA 361
    |||
Db 243 CCGAGAACAGGTCACCCACAGACTGGTGTGAGTGAAGAGTGTCTCTGATGGCGAGGA 302
    |||

QY 362 GATGGACCCGCCAAATCCAGAGGAGGTGAAAAACGCTTGAAGAGGTGAAAAAGCAATCACA 421
    |||
Db 303 GATGGACCCGCCAAATCCAGAGGAGGTGAAAAACGCTTGAAGAGGTGAAAAAGCAATCACA 362
    |||

QY 422 GTGTAAAGAAAGGACAGTTTG 442
    |||
Db 363 GTGTAAAGAAAGGACAGTTTG 383
    |||
```



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 18:20:25 ; Search time 333 Seconds

(without alignments)  
6786.911 Million cell updates/sec

Title: US-09-782-745-17

Perfect score: 532

Sequence: 1 AGCTGTGAGGCGAGTGTGTG.....CTGCAGAGAAAAA 532

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 4998588

Minimum DB seq length: 0

Maximum DB seq length: 532

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*

1: Geneseqn1980s:\*

2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002s:\*

7: Geneseqn2003as:\*

8: Geneseqn2003bs:\*

9: Geneseqn2003cs:\*

10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	532	100.0	532	2	AAX90522 GAGE-5 tu
2	524	98.5	532	2	AAX18720 cDNA enco
3	517.4	97.3	528	6	ABL66323 Lung canc
4	515.8	97.0	527	7	ACC51027 Human bla
5	515.8	97.0	527	7	ABX76236 Lung canc
6	508.8	95.6	526	7	ADA15802 Human GAG
7	504.4	94.8	528	7	ADA15801 Human GAG
8	496.8	93.4	530	7	ABZ20463 GAGE-2 fu
9	350.8	65.9	430	3	AAC02129 Human sec
10	304.6	57.3	530	4	AAS60104 Human can
11	302.4	56.8	365	4	AAS60496 Human can
12	237	44.5	277	7	ABZ19551 Group III
13	235.4	44.2	257	7	ABZ19555 Group III
14	235.4	44.2	264	7	ABZ19755 Group III
15	227.4	42.7	229	7	ABZ20497 TPS1 subt
16	227	42.7	227	7	ABZ20480 TPS1 subt
17	226	42.5	229	7	ABZ18686 Group III
18	211.4	39.7	259	7	ABZ19791 Group III
19	208.4	39.2	520	7	ABZ17937 Human can
20	204	38.3	225	7	ABZ19533 Group III
21	200.8	37.7	509	7	ABX77605 Different
22	200.8	37.7	509	8	ACD42232 Human GAG
23	200.8	37.7	509	9	ADC24646 Human cDN

## ALIGNMENTS

### RESULT 1

AAX90522

ID AAX90522 standard; cDNA; 532 BP.

XX

AC AAX90522;

XX

DT 30-SEP-1999 (first entry)

XX

DE GAGE-5 tumour rejection antigen clone nucleotide sequence.

XX

KW Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection;

KW therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;

KW GAGE; ss.

XX

OS Homo sapiens.

XX

PN WO9937665-A1.

XX

PD 29-JUL-1999.

XX

PF 12-JAN-1999; 99WO-US000775.

XX

PR 23-JAN-1998; 98US-00012818.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Falleur T;

XX

DR WPI; 1999-469111/39.

XX

PT New isolated peptides which bind to HLA-A29 molecules, which are tumor

PT rejection antigens used for detection and therapy of pathological

PT conditions, e.g. cancer.

XX

PS Example 13; Fig 4; 62pp; English.

XX

CC The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic T lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present invention

XX

SQ Sequence 532 BP; 156 A; 111 C; 154 G; 111 T; 0 U; 0 Other;

Query Match 100.0%; Score 532; DB 2; Length 532;  
Best Local Similarity 100.0%; Pred. No. 5.4e-144; Indels 0; Gaps 0;  
Matches 532; Conservative 0; Mismatches 0;

QY 1 AGCTGTGAGGAGTGTGTGGTTCCTGCGTCCGACTCTTTTCTCTACTGAGATT 60  
Db 1 AGCTGTGAGGAGTGTGTGGTTCCTGCGTCCGACTCTTTTCTCTACTGAGATT 60

QY 61 CATCTGTGAAATATAGTGTGGGAGGAGATCGACTATATTATGGCCTAGACCAAGC 120  
Db 61 CATCTGTGAAATATAGTGTGGGAGGAGATCGACTATATTATGGCCTAGACCAAGC 120

QY 121 GCTATGTACAGCTCTCAAGTGTGGCTATGCGCCGAGCAGTTCAGTGAATGAAG 180  
Db 121 GCTATGTACAGCTCTCAAGTGTGGCTATGCGCCGAGCAGTTCAGTGAATGAAG 180

QY 181 TGGAAACAGCAACACCTGAAGAGGGGAACAGCAACTCAACGTCAGGATCCTGAGCTG 240  
Db 181 TGGAAACAGCAACACCTGAAGAGGGGAACAGCAACTCAACGTCAGGATCCTGAGCTG 240

QY 241 CTCAGGAGGAGAGATGAGGAGGATCTGAGGTCAAGGCCGAAGCCTGAAGCTGATA 300  
Db 241 CTCAGGAGGAGAGATGAGGAGGATCTGAGGTCAAGGCCGAAGCCTGAAGCTGATA 300

QY 301 GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGCAGG 360  
Db 301 GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGCAGG 360

QY 361 AGATGGACCCGCCAAATCCAGAGGAGTGAAGACGCTTGAAGAGGTGAAGCAATCAC 420  
Db 361 AGATGGACCCGCCAAATCCAGAGGAGTGAAGACGCTTGAAGAGGTGAAGCAATCAC 420

QY 421 AGTGTAAAGAGGACGCTTGAATGTAGTGAAGCTGCTCTATGTTGGAATTTGTTC 480  
Db 421 AGTGTAAAGAGGACGCTTGAATGTAGTGAAGCTGCTCTATGTTGGAATTTGTTC 480

QY 481 TTAAATTTCTCCCAATAAAGCTTTACAGCCTTTTACAGCCTTTTCAAGAAAAA 532  
Db 481 TTAAATTTCTCCCAATAAAGCTTTACAGCCTTTTACAGCCTTTTCAAGAAAAA 532

RESULT 2  
AAV18720  
ID AAV18720 standard; cDNA; 532 BP.  
XX  
AC AAV18720;  
XX  
DT 30-JUL-1998 (first entry)  
XX  
DE CDNA encoding GAGE-5 tumour rejection antigen precursor.  
XX  
KW GAGE tumour rejection antigen precursor; TRAP; tumour; diagnosis;  
KW melanoma; antigen; cytolytic T cell clone proliferation;  
KW HLA-typing assay; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 75..429  
FT /\*tag= a  
FT /transl\_except= (pos:189..191, aa:Ala)  
FT /transl\_except= (pos:192..194, aa:Thr)  
XX  
FN WO9749417-A1.  
XX  
PD 31-DEC-1997.  
XX  
PF 23-JUN-1997; 97WO-US010850.  
XX  
PR 24-JUN-1996; 96US-00669161.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.

XX Debacker O, Van Den Bynde B, Boon-Falleur T;  
XX WPI; 1998-076905/07.  
DR P-PSDB; AAW47602.  
XX  
XX Isolated nucleic acid encoding GAGE tumour rejection antigen precursor -  
XX processed by HLA-Cw6 molecules into peptides, useful to diagnose  
XX melanomas.  
XX  
XX Example 13; Fig 4; 60pp; English.  
XX  
XX The present sequence encodes a GAGE-5 tumour rejection antigen  
XX precursor (TRAP). The protein is expressed in a number of tumours. In  
XX contrast the only normal tissue which expresses GAGE TRAP protein is  
XX testis. Several GAGE TRAPs have been identified (see AAV18717-21). The  
XX major difference between these proteins and GAGE-1 (AAV05540) is the  
XX absence of a stretch of 143 bases located at position 379 to 521 of the  
XX GAGE-1 TRAP sequence. The rest of the sequences show mismatches at  
XX various positions, with the exception of GAGE-3 whose 5' end is totally  
XX different from the other GAGE cDNAs for the first 112 bases. This region  
XX of GAGE-3 cDNA contains a long repeat and a hairpin structure. The  
XX antigens can be used to diagnose melanomas, characterised by expression  
XX of a TRAP or presentation of a tumour rejection antigen. Antigens shed  
XX into blood or urine can be observed and then used to confirm a diagnosis  
XX of melanoma using cytolytic T cell clone proliferation methodologies.  
XX Other uses for the processed peptides, include HLA-typing assays for,  
XX e.g. skin graft or organ transplants  
XX  
SQ Sequence 532 BP; 154 A; 110 C; 156 G; 112 T; 0 U; 0 Other;  
Query Match 98.5%; Score 524; DB 2; Length 532;  
Best Local Similarity 99.1%; Pred. No. 1.1e-141;  
Matches 527; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AGCTGTGAGGAGTGTGTGGTTCCTGCGTCCGACTCTTTTCTCTACTGAGATT 60  
Db 1 AGCTGTGAGGAGTGTGTGGTTCCTGCGTCCGACTCTTTTCTCTACTGAGATT 60

QY 61 CATCTGTGAAATATAGTGTGGGAGGAGATCGACTATATTATGGCCTAGACCAAGC 120  
Db 61 CATCTGTGAAATATAGTGTGGGAGGAGATCGACTATATTATGGCCTAGACCAAGC 120

QY 121 GCTATGTACAGCTCTCAAGTGTGGCTATGCGCCGAGCAGTTCAGTGAATGAAG 180  
Db 121 GCTATGTACAGCTCTCAAGTGTGGCTATGCGCCGAGCAGTTCAGTGAATGAAG 180

QY 181 TGGAAACAGCAACACCTGAAGAGGGGAACAGCAACTCAACGTCAGGATCCTGAGCTG 240  
Db 181 TGGAAACAGCAACACCTGAAGAGGGGAACAGCAACTCAACGTCAGGATCCTGAGCTG 240

QY 241 CTCAGGAGGAGAGATGAGGAGGATCTGAGGTCAAGGCCGAAGCCTGAAGCTGATA 300  
Db 241 CTCAGGAGGAGAGATGAGGAGGATCTGAGGTCAAGGCCGAAGCCTGAAGCTGATA 300

QY 301 GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGCAGG 360  
Db 301 GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGCAGG 360

QY 361 AGATGGACCCGCCAAATCCAGAGGAGTGAAGACGCTTGAAGAGGTGAAGCAATCAC 420  
Db 361 AGATGGACCCGCCAAATCCAGAGGAGTGAAGACGCTTGAAGAGGTGAAGCAATCAC 420

QY 421 AGTGTAAAGAGGACGCTTGAATGTAGTGAAGCTGCTCTATGTTGGAATTTGTTC 480  
Db 421 AGTGTAAAGAGGACGCTTGAATGTAGTGAAGCTGCTCTATGTTGGAATTTGTTC 480

QY 481 TTAAATTTCTCCCAATAAAGCTTTACAGCCTTTTACAGCCTTTTCAAGAAAAA 532  
Db 481 TTAAATTTCTCCCAATAAAGCTTTACAGCCTTTTACAGCCTTTTCAAGAAAAA 532

ABL66323	ABL66323 standard; DNA; 528 BP.
ID	ABL66323 standard; DNA; 528 BP.
XX	
XX	ABL66323;
XX	
XX	15-MAY-2002 (first entry)
DT	
XX	Lung cancer related gene sequence SEQ ID NO:4660.
XX	
XX	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW	cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW	gene; ds.
KW	
XX	
XX	Homo sapiens.
OS	
XX	
XX	WO200194629-A2.
PN	
XX	
XX	13-DEC-2001.
PD	
XX	
XX	30-MAY-2001; 2001WO-US010838.
XX	
XX	05-JUN-2000; 2000US-0209473P.
PR	
XX	05-JUN-2000; 2000US-0209531P.
PR	
XX	18-SEP-2000; 2000US-0233133P.
PR	
XX	18-SEP-2000; 2000US-0233617P.
PR	
XX	20-SEP-2000; 2000US-0234009P.
PR	
XX	20-SEP-2000; 2000US-0234034P.
PR	
XX	20-SEP-2000; 2000US-0234052P.
PR	
XX	22-SEP-2000; 2000US-0234509P.
PR	
XX	22-SEP-2000; 2000US-0234567P.
PR	
XX	23-SEP-2000; 2000US-0234923P.
PR	
XX	23-SEP-2000; 2000US-0234924P.
PR	
XX	23-SEP-2000; 2000US-0235077P.
PR	
XX	25-SEP-2000; 2000US-0235082P.
PR	
XX	25-SEP-2000; 2000US-0235134P.
PR	
XX	25-SEP-2000; 2000US-0235280P.
PR	
XX	26-SEP-2000; 2000US-0235637P.
PR	
XX	26-SEP-2000; 2000US-0235638P.
PR	
XX	27-SEP-2000; 2000US-0235711P.
PR	
XX	27-SEP-2000; 2000US-0235720P.
PR	
XX	27-SEP-2000; 2000US-0235840P.
PR	
XX	27-SEP-2000; 2000US-0235863P.
PR	
XX	28-SEP-2000; 2000US-0236028P.
PR	
XX	28-SEP-2000; 2000US-0236032P.
PR	
XX	28-SEP-2000; 2000US-0236033P.
PR	
XX	28-SEP-2000; 2000US-0236034P.
PR	
XX	28-SEP-2000; 2000US-0236109P.
PR	
XX	28-SEP-2000; 2000US-0236111P.
PR	
XX	29-SEP-2000; 2000US-0236842P.
PR	
XX	29-SEP-2000; 2000US-0236891P.
PR	
XX	02-OCT-2000; 2000US-0237172P.
PR	
XX	02-OCT-2000; 2000US-0237173P.
PR	
XX	02-OCT-2000; 2000US-0237278P.
PR	
XX	02-OCT-2000; 2000US-0237294P.
PR	
XX	02-OCT-2000; 2000US-0237295P.
PR	
XX	02-OCT-2000; 2000US-0237316P.
PR	
XX	03-OCT-2000; 2000US-0237425P.
PR	
XX	03-OCT-2000; 2000US-0237598P.
PR	
XX	03-OCT-2000; 2000US-0237604P.
PR	
XX	03-OCT-2000; 2000US-0237606P.
PR	
XX	03-OCT-2000; 2000US-0237608P.
PR	
XX	01-NOV-2000; 2000US-0244867P.
PR	
XX	01-NOV-2000; 2000US-0245084P.
PR	
XX	
XX	(AVAL-) AVALON PHARM.
PA	
XX	
XX	Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI	Soppet DR, Weaver Z;
PI	
XX	
XX	WPI; 2002-188264/24.
DR	
XX	
XX	Screening for anti-neoplastic agent involves exposing cells to a chemical

XX DE Human bladder cancer associated cDNA sequence SEQ ID NO:144.  
 XX KW Human; bladder cancer; cytostatic; gene therapy; vaccine; gene; ss.  
 XX OS Homo sapiens.  
 XX PN W02003003906-A2.  
 XX PD 16-JAN-2003.  
 XX PF 03-JUL-2002; 2002WO-US021338.  
 XX PR 03-AUG-2001; 2001US-0302814P.  
 XX PR 08-NOV-2001; 2001US-0310099P.  
 XX PR 13-NOV-2001; 2001US-0343705P.  
 XX PR 12-APR-2002; 2002US-0350666P.  
 XX PR 12-APR-2002; 2002US-0372246P.  
 XX PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 XX PI Mack DH, Aziz N;  
 XX PI WPI; 2003-201532/19.  
 XX DR P-PSDB; ABR48213.  
 XX DR  
 XX PT Detecting a bladder cancer-associated transcript in a cell from a  
 PT patient, comprises contacting a biological sample from the patient with a  
 PT bladder cancer-associated polynucleotide or antibody.  
 XX PS Claim 6; Page 279; 307pp; English.  
 XX CC The present invention describes a method for detecting a bladder cancer-  
 CC associated transcript in a cell from a patient. The method comprises  
 CC contacting a biological sample from the patient with a polynucleotide  
 CC that selectively hybridizes to a sequence that is 80 % identical to a  
 CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059  
 CC encode the human bladder cancer-associated proteins given in ABR48146 to  
 CC ABR48242). Bladder cancer-associated sequences from the present invention  
 CC have cytostatic activities, and can be used in antisense gene therapy and  
 CC in vaccine production. The method can be used for detecting a bladder  
 CC cancer-associated transcript in a cell from a patient. The method is  
 CC useful in diagnosing or treating bladder cancer and in screening for  
 CC compounds that modulate bladder cancer, such as hormones or antibodies.  
 CC The nucleic acid molecules from the present invention may be used in  
 CC various screening and diagnostic methods, and for gene therapy, vaccine  
 CC and/or antisense/inhibition applications  
 XX SQ Sequence 527 BP; 146 A; 113 C; 157 G; 111 T; 0 U; 0 Other;  
 Query Match 97.0%; Score 515.8; DB 7; Length 527;  
 Best Local Similarity 99.6%; Pred. No. 2.7e-139;  
 Matches 517; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 AGCTGTGAGGCGAGTGTGTGTTCTGCTGCGTCCGGACTCTTTTCTCTACTGAGATT 60  
 Db |||||||  
 QY 8 AGCTGTGAGGCGAGTGTGTGTTCTGCTGCGTCCGGACTCTTTTCTCTACTGAGATT 67  
 |||||||  
 QY 61 CATCTGTGTGAATATGAGTGTGCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGC 120  
 Db |||||||  
 QY 68 CATCTGTGTGAATATGAGTGTGCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGC 127  
 |||||||  
 QY 121 GCTATGTACAGCTCTGTAAGTGAATGGCCCTATGCGGCCGAGGAGTTCAGTGTGAAG 180  
 Db |||||||  
 QY 128 GCTATGTACAGCTCTGTAAGTGAATGGCCCTATGCGGCCGAGGAGTTCAGTGTGAAG 187  
 |||||||  
 QY 181 TCGAACCCAGCAACCTGAGAGGGGACACGACCTCAAGTTCAGGATCTCTGAGCTG 240  
 Db |||||||  
 QY 188 TCGAACCCAGCAACCTGAGAGGGGACACGACCTCAAGTTCAGGATCTCTGAGCTG 247  
 |||||||  
 QY 241 CTCAGAGGGGAGGAGTATGAGGAGCATCTGCAAGGTCAAGGGCCGAGCTGAAGCTGATA 300  
 Db |||||||  
 QY 248 CTCAGAGGGGAGGAGTATGAGGAGCATCTGCAAGGTCAAGGGCCGAGCTGAAGCTGATA 307  
 |||||||

QY 301 GCCAGGAACAGGCTCACCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGCAGG 360  
 Db |||||||  
 QY 308 GCCAGGAACAGGCTCACCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGCAGG 367  
 |||||||  
 QY 361 AGATGGACCCGCCCAATCCAGAGAGGTGAAAACGCCCTGAAGAGGTGAAAAGCAATCAC 420  
 Db |||||||  
 QY 368 AGGTGGACCCGCCCAATCCAGAGAGGTGAAAACGCCCTGAAGAGGTGAAAAGCAATCAC 427  
 |||||||  
 QY 421 AGTGTAAAGAGGCGACGTTGAAATGATCGACGCTCTCTATGTTGGAAATTTGTTC 480  
 Db |||||||  
 QY 428 AGTGTAAAGAGGACACACGTTGAAATGATCGACGCTCTCTATGTTGGAAATTTGTTC 487  
 |||||||  
 QY 481 TTAATAATCTCCCAATAAAGCTTTACAGCCCTTCGCAAA 519  
 Db |||||||  
 QY 488 TTAATAATCTCCCAATAAAGCTTTACAGCCCTTCGCAAA 526  
 |||||||  
 RESULT 5  
 ABX76236  
 ID ABX76236 standard; DNA; 527 BP.  
 XX AC ABX76236;  
 XX DT 02-APR-2003 (first entry)  
 XX DE Lung cancer-associated polynucleotide #105.  
 XX KW Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;  
 KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;  
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;  
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;  
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.  
 XX OS Unidentified.  
 XX PN W0200286443-A2.  
 XX PD 31-OCT-2002.  
 XX PF 18-APR-2002; 2002WO-US012476.  
 XX PR 18-APR-2001; 2001US-0284770P.  
 XX PR 10-MAY-2001; 2001US-0290492P.  
 XX PR 09-NOV-2001; 2001US-0339245P.  
 XX PR 13-NOV-2001; 2001US-0350666P.  
 XX PR 29-NOV-2001; 2001US-0334370P.  
 XX PR 12-APR-2002; 2002US-0372246P.  
 XX PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 XX PI Aziz N, Murray R;  
 XX PI WPI; 2003-093161/08.  
 XX DR P-PSDB; ABUS6512.  
 XX PT Detecting a lung cancer-associated transcript in a cell from a patient  
 PT for treating lung cancer, by contacting a biological sample from the  
 PT patient with a polynucleotide that exhibits increased or decreased  
 PT expression in lung cancer.  
 XX PS Claim 22; Page 273; 453pp; English.  
 XX CC The invention relates to a method for detecting a lung cancer-associated  
 CC transcript in a cell from a patient, comprising contacting a biological  
 CC sample from the patient with a polynucleotide that selectively hybridizes  
 CC to a sequence that is at least 80 % identical to a gene that exhibits  
 CC increased or decreased expression in lung cancer samples. Lung cancer-  
 CC associated polynucleotides and polypeptides are used for identifying a  
 CC compound that modulates a lung cancer-associated polypeptide, for  
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung  
 CC cancer in a patient and for treating a mammal having lung cancer by  
 CC administering a modulatory compound identified. The methods are useful

CC for treating lung cancer, such as small cell lung cancer, non-small cell  
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,  
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,  
 CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and  
 CC bronchiectasis. The genes, polynucleotides and polypeptides are useful  
 CC for diagnostic purposes and as targets for screening for therapeutic  
 CC compounds that modulate lung cancer, such as antibodies. Sequences  
 CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the  
 CC invention  
 XX  
 XX  
 SQ Sequence 527 BP; 146 A; 113 C; 157 G; 111 T; 0 U; 0 Other;

Query Match 97.0%; Score 515.8; DB 7; Length 527;  
 Best Local Similarity 99.6%; Pred. No. 2.7e-137;  
 Matches 517; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 AGCTGTGAGGAGTCTGTGTGTTCTTCCGCTCCGAGTCTTTTCTCTACTCAGATT 60  
 DB |||||  
 DB 8 AGCTGTGAGGAGTCTGTGTGTTCTTCCGCTCCGAGTCTTTTCTCTACTCAGATT 67  
 QY 61 CATCTGTGAAATATGATTGGCGAGGAAGATGACCTATTATTGGCTAGACCAAGGC 120  
 DB |||||  
 DB 68 CATCTGTGAAATATGATTGGCGAGGAAGATGACCTATTATTGGCTAGACCAAGGC 127  
 QY 121 GCTATGTACAGCTCTCAAGTGATTGGGCTTATCGGCCGAGCAGTTCAGTGATGAAG 180  
 DB |||||  
 DB 128 GCTATGTACAGCTCTCAAGTGATTGGGCTTATCGGCCGAGCAGTTCAGTGATGAAG 187  
 QY 181 TGGAAACCAACACCTCTGAAGAGGGGACCAAGCAACTCAAGTCAAGTCTCAGCTG 240  
 DB |||||  
 DB 188 TGGAAACCAACACCTCTGAAGAGGGGACCAAGCAACTCAAGTCAAGTCTCAGCTG 247  
 QY 241 CTCAGAGGAGAGATGAGGAGATCTGCAAGTCAAGGCGGAGGCTGAAGCTGATA 300  
 DB |||||  
 DB 248 CTCAGAGGAGAGATGAGGAGATCTGCAAGTCAAGGCGGAGGCTGAAGCTGATA 307  
 QY 301 GCCAGGAACAGGTCACCCACAGACTGGGTGTGAGTGCAAGATGCTGTGATGGCAGG 360  
 DB |||||  
 DB 308 GCCAGGAACAGGTCACCCACAGATGGGTGTGAGTGCAAGATGCTGTGATGGCAGG 367  
 QY 361 AGATGGACCCGCAATCCAGAGGAGGTGAACACGCTGAAGAGGTGAAGAGCAATCAC 420  
 DB |||||  
 DB 368 AGGTGACCCGCAATCCAGAGGAGGTGAACACGCTGAAGAGGTGAAGAGCAATCAC 427  
 QY 421 AGTGTAAAGAGGACGTTGAATGATGCAAGGCTGCTCTATGTTGAAATTTGTTCA 480  
 DB |||||  
 DB 428 AGTGTAAAGAGGACGTTGAATGATGCAAGGCTGCTCTATGTTGAAATTTGTTCA 487  
 QY 481 TTAAATTTCTCCCAATAAGCTTTACAGCTTCTGCAA 519  
 DB |||||  
 DB 488 TTAAATTTCTCCCAATAAGCTTTACAGCTTCTGCAA 526

RESULT 6  
 ID ADA15802  
 XX ADA15802 standard; cDNA; 526 BP.  
 AC ADA15802;  
 XX  
 XX 06-NOV-2003 (first entry)  
 XX Human GAGE-7B cDNA.  
 XX Human; GAGE-7B; gene; ss; cytolytic T lymphocyte; CTL;  
 KW human leukocyte antigen; HLA; tumour rejection antigen precursor;  
 KW major histocompatibility complex; MHC; cytolytic T cell proliferation;  
 KW chromosome Xp11.2-p11.4.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH 55..408  
 FT CDS /\*tag= a  
 FT

FT  
 FT  
 FT  
 XX  
 PN  
 XX  
 PD  
 XX  
 PF  
 XX  
 PR  
 XX  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 PI De Backer O, Van Den Eynde B, Boon-Falleur T;  
 XX  
 WPI; 2003-401119/38.  
 P-PSDB; ADA15777.  
 XX  
 PT New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tumor  
 PT rejection antigen precursors, which complex to major histocompatibility  
 PT complex molecules to facilitate the proliferation of cytolytic T cells.  
 XX  
 PS Claim 1; Col 9-10; 15pp; English.  
 CC The invention relates to isolated GAGE-7B and GAGE-8 polypeptides and the  
 CC nucleic acid molecules encoding them. The invention also relates to an  
 CC expression vector comprising an isolated nucleic acid molecule of the  
 CC invention operably linked to a promoter, a recombinant cell comprising  
 CC the isolated nucleic acid molecule or the expression vector and an  
 CC expression kit useful in generating cytolytic T lymphocytes (CTLs) or  
 CC determining if CTLs are present in a sample comprising the isolated  
 CC nucleic acid molecule and the isolated nucleic acid that encodes a human  
 CC leukocyte antigen (HLA) molecule. The GAGE-7B and GAGE-8 nucleic acid  
 CC molecules encode tumour rejection antigen precursors, which complex to  
 CC major histocompatibility complex (MHC) molecules to facilitate the  
 CC proliferation of cytolytic T cells. This sequence represents cDNA  
 CC encoding the human GAGE-7B polypeptide of the invention. The gene resides  
 CC on chromosome Xp11.2-p11.4.  
 XX  
 SQ Sequence 526 BP; 168 A; 109 C; 143 G; 106 T; 0 U; 0 Other;

Query Match 95.6%; Score 508.8; DB 7; Length 526;  
 Best Local Similarity 99.6%; Pred. No. 2.9e-137;  
 Matches 510; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 21 TGGTTCCTGCGCTCGGACTCTTTTCTCTACTGAGATTCTGTGTGAAATATGAGT 80  
 DB |||||  
 DB 1 TGGTTCCTGCGCTCGGACTCTTTTCTCTACTGAGATTCTGTGTGAAATATGAGT 60  
 QY 81 TGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTCTGAA 140  
 DB |||||  
 DB 61 TGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTCTGAA 120  
 QY 141 GTGATTGGCGCTTATCGGCCGAGCAGTTTCACTGATGAAGTGGAACACAGCACTGAA 200  
 DB |||||  
 DB 121 ATGATTGGCGCTTATCGGCCGAGCAGTTTCACTGATGAAGTGGAACACAGCACTGAA 180  
 QY 201 GAAGGGGAACCAAGCAACTCAAGCTCAGGATCCTGAGCTGTCTCAGAGGGAGAGATGAG 260  
 DB |||||  
 DB 181 GAAGGGGAACCAAGCAACTCAAGCTCAGGATCCTGAGCTGTCTCAGAGGGAGAGATGAG 240  
 QY 261 GGAGCATCTGAGGTCAAGGGCCGAGCTGAAGCTGATGAGCCAGGAACAGGTTACCCCA 320  
 DB |||||  
 DB 241 GGAGCATCTGAGGTCAAGGGCCGAGCTGAAGCTGATGAGCCAGGAACAGGTTACCCCA 300  
 QY 321 CAGACTGGGTGTGAGTGTGAAGATGCTCTGATGGCAGGAGATGAGCCGCCAAATCCA 380  
 DB |||||  
 DB 301 CAGACTGGGTGTGAGTGTGAAGATGCTCTGATGGCAGGAGATGAGCCGCCAAATCCA 360  
 QY 381 GAGGAGGTGAACACGCTCAAGAGAGGTGAAGAGCAATCACAGTGTAAAGAGGACGCT 440  
 DB |||||  
 DB 361 GAGGAGGTGAACACGCTCAAGAGAGGTGAAGAGCAATCACAGTGTAAAGAGGACGCT 420

/product= "Human GAGE-7B"  
 /transl\_except= (pos:115..162, aa: GPMREPGSGDEVPEMI)  
 /transl\_except= (pos:265..306, aa: HPQTKPRAHSQEQ)

QY 441 TGAATGATGAGGCTCTCTATGTTGGAAATTTGTTCAATAAATTTCTCCCAATAAG 500  
 |||||  
 Db 421 TGAATGATGAGGCTCTCTATGTTGGAAATTTGTTCAATAAATTTCTCCCAATAAG 480  
 |||||  
 QY 501 CTTTACAGCCTTCTGCAAGAAAAA 532  
 |||||  
 Db 481 CTTTACAGCCTTCTGCAAGAAAAA 512  
 |||||

## RESULT 7

ADAL5801

ID ADAL5801 standard; cDNA; 528 BP.

XX AC

ADA15801;

XX DT

06-NOV-2003 (first entry)

XX DE

Human GAGE-8 cDNA.

XX KW

Human; GAGE-8; gene; ss; cytolytic T lymphocyte; CTL;

KW human leukocyte antigen; HLA; tumour rejection antigen precursor;

KW major histocompatibility complex; MHC; cytolytic T cell proliferation;

KW chromosome Xp11.2-p11.4.

XX OS

Homo sapiens.

XX FH

Key Location/Qualifiers

CDS 73..423

/\*tag= a

/product= "Human GAGE-8"

/transl\_except= (pos:244..246, aa:Gln)

/transl\_except= (pos:400..402, aa:Lys)

XX FT

US6509172-B1.

XX PN

XX PD

21-JAN-2003.

XX PF

30-SEP-1998; 98US-00163748.

XX PP

30-SEP-1998; 98US-00163748.

XX PR

(LUDW-) LUDWIG INST CANCER RES.

XX PA

De Backer O, Van Den Eynde B, Boon-Falleur T;

XX PI

WPI; 2003-401119/38.

XX DR

P-PSDB; ADA15778.

XX DR

XX PT

XX PT

XX PT

XX PT

XX PT

XX PT

XX PS

Claim 1; Col 7-10; 15pp; English.

XX CC

The invention relates to isolated GAGE-7B and GAGE-8 polypeptides and the nucleic acid molecules encoding them. The invention also relates to an expression vector comprising an isolated nucleic acid molecule of the invention operably linked to a promoter, a recombinant cell comprising the isolated nucleic acid molecule or the expression vector and an expression kit useful in generating cytolytic T lymphocytes (CTLs) or determining if CTLs are present in a sample comprising the isolated nucleic acid molecule and the isolated nucleic acid that encodes a human leukocyte antigen (HLA) molecule. The GAGE-7B and GAGE-8 nucleic acid molecules encode tumour rejection antigen precursors, which complex to major histocompatibility complex (MHC) molecules to facilitate the proliferation of cytolytic T cells. This sequence represents cDNA encoding the human GAGE-8 polypeptide of the invention. The gene resides on chromosome Xp11.2-p11.4.

XX CC

Sequence 528 BP; 158 A; 112 C; 151 G; 107 T; 0 U; 0 Other;

XX SQ

Query Match

94.8%; Score 504.4; DB 7; Length 528;

Best Local Similarity 98.3%; Pred. No. 5.5e-136;  
 Matches 521; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

QY 3 CTGTGAGGCAAGTGTCTGTGTGGTTCCTGCGCCCTCGGACTCTTTTCTCTCTAGATCA 62

Db 1 CTGTGAGGCAAGTGTCTGTGTGGTTCCTGCGCCCTCGGACTCTTTTCTCTCTAGATCA 60

QY 63 TCTGTGTGAAATATGAGTTGGCGGAGGAAGATGACCTATTATTGGCCCTAGACCAAGGCGC 122

Db 61 TCTGTGTGAAATATGAGTTGGCGGAGGAAGATGACCTATTATTGGCCCTAGACCAAGGCGC 117

QY 123 TATGTACAGCCTCTCTGAAAGTATTGGGCCCTATGCGGCCCGGAGCAGTTCAGTGATGAAGTG 182

Db 118 TACGTAGAGCCTCTCTGAAATGATTGGGCCCTATGCGGCCCGGAGCAGTTCAGTGATGAAGTG 177

QY 183 GAACCAAGCAACCTCTGAAAGGGAACCAAGCAACTCAACGTCAGGATCCTGCAAGCTGCT 242

Db 178 GAACCAAGCAACCTCTGAAAGGGAACCAAGCAACTCAACGTCAGGATCCTGCAAGCTGCT 237

QY 243 CAGGAGGAGGAGATGAGGAGGAGCATCTGCAGGTCAAGGGCCGAGGCTGAAGCTGATAGC 302

Db 238 CAGGAGGAGGAGATGAGGAGGAGCATCTGCAGGTCAAGGGCCGAGGCTGAAGCTGATAGC 297

QY 303 CAGGAAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGGCAAGAG 362

Db 298 CAGGAAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGGCAAGAG 357

QY 363 ATGGACCCGCCAAATCCAGAGGAGGTGAAGCCCTGAAGAGGTGAAGAGCAATCAAG 422

Db 358 ATGGACCCGCCAAATCCAGAGGAGGTGAAGCCCTGAAGAGGTGAAGAGCAATCAAG 417

QY 423 TGTATAAAGAGGACGCTTGAATGATGCAAGGCTGCTCTCTATGTTGGAATTTGTTCAAT 482

Db 418 TGTATAAAGAGGACGCTTGAATGATGCAAGGCTGCTCTCTATGTTGGAATTTGTTCAAT 477

QY 483 AAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA 532

Db 478 AAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA 527

RESULT 8

ABZ20463

ID ABZ20463 standard; cDNA; 530 BP.

XX AC

ABZ20463;

XX DT

23-JAN-2003 (first entry)

XX DE

GAGE-2 full length cDNA sequence SEQ ID NO:2890.

XX KW

Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;

KW immune response; virology; immunology; microbiology; molecular biology;

KW recombinant DNA technology; gene; ss.

XX OS

Homo sapiens.

XX PN

WO200278516-A2.

XX PD

10-OCT-2002.

XX PF

28-MAR-2002; 2002WO-US010421.

XX PR

30-MAR-2001; 2001US-0280255P.

XX PR

28-AUG-2001; 2001US-0315563P.

XX PR

09-JAN-2002; 2002US-0347313P.

XX PA

(CORI-) CORIXA CORP.

XX PI

Wang T, Wang S, Bangur CS, Gaiger A;

XX DR

WPI; 2003-058387/05.

XX DR

P-PSDB; ABP54447.

PT New immunogenic polynucleotides or polypeptides useful for diagnosing,  
PT preventing and treating cancer expressing CT or CP mRNA antigens, and in  
PT virology, immunology, microbiology, molecular biology and recombinant DNA  
PT techniques.

XX Claim 1; SEQ ID NO 2890; 207pp; English.

XX ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and  
CC ABP54446 to ABP54472 represent protein (II) sequences, from the present  
CC invention. (I) and (II) have cytostatic activity and can be used in gene  
CC therapy and vaccines. (I), (II), antibodies and compositions from the  
CC present invention are useful for diagnosing, preventing and treating  
CC cancer, which expresses CT or CP mRNA antigens. They are useful for  
CC stimulating immune response. They can also be useful in virology,  
CC immunology, microbiology, molecular biology and recombinant DNA  
CC techniques. N.B. The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 530 BP; 152 A; 116 C; 155 G; 107 T; 0 U; 0 Other;

Query Match 93.4%; Score 496.8; DB 7; Length 530;

Best Local Similarity 98.1%; Pred. No. 8.9e-134;

Matches 514; Conservative 0; Mismatches 7; Indels 3; Gaps 1;

QY 1 AGCTGTGAGGAGTGTGTGTGTTCTCGCTCGGACTCTTTTCTCTACTGAGATT 60

Db 10 AGCTGTGAGGAGTGTGTGTGTTCTCGCTCGGACTCTTTTCTCTACTGAGATT 69

QY 61 CATCTGTGTGAATATGATTCGCGAGGAAGATCGACCTATTATGGCCCTAGACCAAGGC 120

Db 70 CATCTGTGTGAATATGATTCGCGAGGAAGATCGACCTATTATGGCCCTAGACCAAGGC 126

QY 121 GGTATGTACAGCTCTGTGAAGTATTTGGCCCTATGCGGCCGAGCAGTTCATGTATGAAG 180

Db 127 GCTACGTAGAGCTCTCTGAATGATTTGGCCCTATGCGGCCGAGCAGTTCATGTATGAAG 186

QY 181 TGGAAACAGCACACTGGAAGAGGGACACGACCTCAACGTGAGGATCTCGAGCTG 240

Db 187 TGGAAACAGCACACTGGAAGAGGGACACGACCTCAACGTGAGGATCTCGAGCTG 246

QY 241 CTCAGGAGGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAGCCTGAAGCTGATA 300

Db 247 CTCAGGAGGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAGCCTGAAGCTCATA 306

QY 301 GCCAGAACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGTATGGCAGG 360

Db 307 GCCAGAACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGTATGGCAGG 366

QY 361 AGATGACCCGCAATCCAGAGGAGGTGAACCCCTCAAGAGGTGAAGAGCAATCAC 420

Db 367 AGATGACCCGCAATCCAGAGGAGGTGAACCCCTCAAGAGGTGAAGAGCAATCAC 426

QY 421 AGTGTATAAAGAGGCACCTTGAATGATGACGGCTGCTCTATGTTGAAATTTGTTCA 480

Db 427 AGTGTATAAAGAGGCACCTTGAATGATGACGGCTGCTCTATGTTGAAATTTGTTCA 486

QY 481 TTAAATTTCTCCATATAAGCTTTACAGCTTCTGCAAGAAAA 524

Db 487 TTAAATTTCTCCATATAAGCTTTACAGCTTCTGCAAGAAAA 530

RESULT 9

AAC02129

ID AAC02129 standard; cDNA; 430 BP.

XX AAC02129;

XX 06-OCT-2000 (first entry)

DE Human secreted protein 5' EST, SEQ ID NO: 2127.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

gene therapy; chromosome mapping; ss.

XX Homo sapiens.

XX EP1033401-A2.

PD 06-SEP-2000.

XX 21-FEB-2000; 2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

XX (GEST ) GENSET.

PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

DR P-PSDB; AAG02123.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX Claim 1; SEQ ID NO 2127; 71pp + Sequence Listing; English.

CC The present sequence is one of a large number of 5' ESTs derived from  
CC mRNAs encoding secreted proteins. An ORF has been identified within the  
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs  
CC derived from 30 different tissues. EST sequences usually correspond  
CC mainly to the 3' untranslated region (UTR) of the mRNA because they are  
CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not  
CC well suited for isolating cDNA sequences derived from the 5' ends of  
CC mRNAs and even in those cases where longer cDNA sequences have been  
CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from  
CC mRNAs with intact 5' ends and can therefore be used to obtain full length  
CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,  
CC gene therapy and chromosome mapping procedures. They are used to obtain  
CC upstream regulatory sequences and to design expression and secretion  
CC vectors

XX SQ Sequence 430 BP; 101 A; 102 C; 134 G; 85 T; 0 U; 8 Other;

Query Match 65.9%; Score 350.8; DB 3; Length 430;

Best Local Similarity 97.6%; Pred. No. 1.9e-91;

Matches 360; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

QY 1 AGCTGTGAGGAGTGTGTGTGTTCTCGCTCGGACTCTTTTCTCTACTGAGATT 60

Db 63 AGCTGTGAGGAGTGTGTGTGTTCTCGCTCGGACTCTTTTCTCTACTGAGATT 122

QY 61 CATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATTATTTGGCTAGACCAAGGC 120

Db 123 CATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATTATTTGGCTAGACCAAGGC 181

QY 121 GCTATGTACGCTCTCAAGTGTATGGCTATGCGGCCGAGCAGTTCAGTGTGAAG 180

Db 182 GCTATGTACGCTCTCAAGTGTATGGCTATGCGGCCGAGCAGTTCAGTGTGAAG 241

QY 181 TGGAAACAGCAACCTCGAAGAGGGGAACAGCAACTCAACGTGAGGATCTGCGAGCTG 240

Db 242 TGGAAACAGCAACCTCGAAGAGGGGAACAGCAACTCAACGTGAGGATCTGCGAGCTG 301

QY 241 CTCAGGAGGAGGATGAGGAGCATCTGAGGTCAAGGGCCGAGCCTGAAGCTGATA 300

Db 302 CTCAGGAGGAGGATGAGGAGCATCTGAGGTCAAGGGCCGAGCCTGAAGCTGATA 361

QY 301 GCCAGAACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGTATGGCAGG 360

Db 362 GCCAGAACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGTATGGCAGG 421

QY 361 AGATGGACC 369

Db 422 AGATGGACC 430

Qy	349	CTGATGGGCGAGGATGGACCCGCCAAATCCAGAGGAGGTGAAAAGCGCTGAAGAAGGTG	408
ID	AAS60104	standard; cDNA; 530 BP.	
XX			
AC	AAS60104;		
XX			
DT	29-JAN-2002	(first entry)	
XX			
DE	Human cancer agent-sensitive marker #105.		
XX			
KW	Human; cancer cell marker; TAXOL; cytostatic; tumour; carcinoma;		
KW	squamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia;		
KW	lymphocytic leukaemia; lymphoma; plasmocytoma; reticulum cell sarcoma;		
KW	Hodgkin's disease; glioma; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200179556-A2.		
XX			
PD	25-OCT-2001.		
XX			
PF	13-APR-2001; 2001WO-US012132.		
XX			
PR	14-APR-2000; 2000US-0197538P.		
XX			
PA	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.		
XX			
PI	Lillie J, Brown JL, Bolt A, Van Huffel C;		
XX			
DR	WPI; 2001-602933/69.		
XX			
PT	Novel nucleic acid, used as a marker to determine the effectiveness of		
PT	using TAXOL to treat cancer cell growth in individuals.		
XX			
PS	Claim 1; Page 120; 527pp; English.		
XX			
CC	The invention relates to 1046 novel nucleic acids which are used as		
CC	markers for determining the sensitivity of a cancer cell to the		
CC	anticancer agent TAXOL. Cancer cells can be treated with TAXOL when they		
CC	are shown to express one of the 242 sensitivity markers or the cells are		
CC	shown not to express one of the 804 resistance markers. The methods can		
CC	be used to determine the effectiveness of TAXOL in the treatment of		
CC	cancer cell growth in an individual. The markers can be used as targets		
CC	in developing anti-cancer agents such as chemotherapeutic compounds. The		
CC	markers can also be used as targets in developing treatments for cancer,		
CC	particularly those cancers which display resistance to agents and exhibit		
CC	expression of the markers. The anticancer agents developed by the novel		
CC	method can be used to treat cancer. Probes based on the markers can be		
CC	used to detect transcripts or genomic sequences corresponding to the		
CC	markers, in the identification of cells or tissues which mis-express the		
CC	protein. Cancers which may be targeted include carcinoma (e.g. squamous		
CC	cell carcinoma), sarcoma (e.g. fibrosarcoma) leukaemia (e.g. lymphocytic		
CC	leukaemia), lymphoma, plasmocytoma, reticulum cell sarcoma, Hodgkin's		
CC	disease and tumours (e.g. glioma). The present sequence is one of the		
CC	1046 novel cancer cell markers		
XX			
SQ	Sequence 530 BP; 89 A; 100 C; 106 G; 183 T; 0 U; 52 Other;		
	Query Match 57.3%; Score 304.6; DB 4; Length 530;		
	Best Local Similarity 88.5%; Pred. No. 5.4e-78;		
	Matches 332; Conservative 0; Mismatches 40; Indels 2; Gaps 1;		
Qy	171	AGTGATGAGTGAACACAGC--AACACCTGAAGAGGGGAAACAGCAACTCAACCTCAGG	228
Db	449	AGTNATNAAGTGACCCANCNCNCCCTGAANAAGGNAACAGCAACTCAACCTNAGG	390
Qy	229	ATCCTCAGCTGCTCAGGAGGGAGAGCAGGAGCATCTCAGTCAAGGCCGAGAC	288
Db	389	ATCCTGNAGCTGCNAGNAGGAGGAGATNAGGNGCATNTCAGTCAAGGCCGAGAC	330
Qy	289	CTGAAGCTGATACCCAGGAACAGGGGTACCCACAGACTGGGTGTGAGTGTGAAGATGTC	348



CC disease and tumours (e.g. glioma). The present sequence is one of the  
CC 1046 novel cancer cell markers  
XX  
SQ Sequence 365 BP; 63 A; 86 C; 66 G; 150 T; 0 U; 0 Other;  
Query Match 56.8%; Score 302.4; DB 4; Length 365;  
Best Local Similarity 96.6%; Pred. No. 2e-77;  
Matches 309; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 213 GCACCTCAGCGTCAGGATCTGACGCTGCTCAGGAGGAGAGATGAGGAGCATCTGCA 272  
Db |||||  
365 GCACCTCAGCGTCAGGATCTGACGCTGCTCAGGAGGAGAGATGAGGAGCATCTGCA 306  
QY 273 GGTCAGGGCCGGAAGCCTGAAGCTGATAGCCAGGAACAGGTCACCCACAGACTGGGTGT 332  
Db |||||  
305 GGTCAGGGCCGGAAGCCTGAAGCTGATAGCCAGGAACAGGTCACCCACAGACTGGGTGT 246  
QY 333 GAGTGTGAAGATGGTCTCTGATGGCGAGGAGATGACCCGCCAAATCCAGAGAGGTGAAA 392  
Db |||||  
245 GAGTGTGAAAATGGTCTCTGATGGCGAGGAAATGACCCGCCAAATCCAAAGGAGGTGAAA 186  
QY 393 AGCCCTGAAGAGGTGAAAAGCAATCACAGTGTATAAAGAGGCAGGTTGAAATGATGCA 452  
Db |||||  
185 AGCCCTGAAGAGGTGAAAAGCAATCTCAGTGTATAAAGAGGCAGGTTGAAATGATGCA 126  
QY 453 GGCTGCTCCTATGTTGGAATTTGTTCAATTAAAAATTTCTCCCAATAAGCTTTACAGCCTT 512  
Db |||||  
125 GGCTGCTCCTATGTTGGAATTTGTTCAATTAAAAATTTCTCCCAATAAGCTTTACAGCCTT 66  
QY 513 CTGCAAGAAAAA 532  
Db |||||  
65 CTAAGAAAAA 46

RESULT 12  
ABZ19551/c  
ID ABZ19551 standard; cDNA; 277 BP.  
XX  
AC ABZ19551;  
XX  
DT 23-JAN-2003 (first entry)  
XX  
DE Group III cDNA cancer related clone SEQ ID NO:1977.  
XX  
DE Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;  
KW immune response; virology; immunology; microbiology; molecular biology;  
KW recombinant DNA technology; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200278516-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 28-MAR-2002; 2002WO-US010421.  
XX  
PR 30-MAR-2001; 2001US-0280255P.  
PR 28-AUG-2001; 2001US-0315563P.  
PR 09-JAN-2002; 2002US-0347313P.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Wang T, Wang S, Bangur CS, Gaiger A;  
PI WPI; 2003-058387/05.  
XX  
DR New immunogenic polynucleotides or polypeptides useful for diagnosing,  
PT preventing and treating cancer expressing CT or CP mRNA antigens, and in  
PT virology, immunology, microbiology, molecular biology and recombinant DNA  
PT techniques.  
XX  
PS Claim 1; SEQ ID NO 1977; 207pp; English.  
XX

CC ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and  
CC ABP54446 to ABP54472 represent protein (II) sequences, from the present  
CC invention. (I) and (II) have cytostatic activity and can be used in gene  
CC therapy and vaccines. (I), (II), antibodies and compositions from the  
CC present invention are useful for diagnosing, preventing and treating  
CC cancer, which expresses CT or CP mRNA antigens. They are useful for  
CC stimulating immune response. They can also be useful in virology,  
CC immunology, microbiology, molecular biology and recombinant DNA  
CC techniques. N.B. The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 277 BP; 62 A; 79 C; 73 G; 63 T; 0 U; 0 Other;  
Query Match 44.5%; Score 237; DB 7; Length 277;  
Best Local Similarity 100.0%; Pred. No. 1.6e-58;  
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTGTGAGGCGAGTGTGTGTCTCTGCTCCCTCGGACTCTTTTCTCTACTGAGATT 60  
Db |||||  
237 AGCTGTGAGGCGAGTGTGTGTCTCTGCTCCCTCGGACTCTTTTCTCTACTGAGATT 178  
QY 61 CATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGGC 120  
Db |||||  
177 CATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGGC 118  
QY 121 GCTATGTACAGCTCTCTGAAAGTATGGGCTTATGGGCCCGAGCAGTTTCAGTGTAGAG 180  
Db |||||  
117 GCTATGTACAGCTCTCTGAAAGTATGGGCTTATGGGCCCGAGCAGTTTCAGTGTAGAG 58  
QY 181 TGGAAACCGACACCTGAGAGGAGGAAACCGAGCAACTCAAGTCAGGATCCTGCAG 237  
Db |||||  
57 TGGAAACCGACACCTGAGAGGAGGAAACCGAGCAACTCAAGTCAGGATCCTGCAG 1

RESULT 13  
ABZ19955/c  
ID ABZ19955 standard; cDNA; 257 BP.  
XX  
AC ABZ19955;  
XX  
DT 23-JAN-2003 (first entry)  
XX  
DE Group III cDNA cancer related clone SEQ ID NO:2381.  
XX  
DE Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;  
KW immune response; virology; immunology; microbiology; molecular biology;  
KW recombinant DNA technology; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200278516-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 28-MAR-2002; 2002WO-US010421.  
XX  
PR 30-MAR-2001; 2001US-0280255P.  
PR 28-AUG-2001; 2001US-0315563P.  
PR 09-JAN-2002; 2002US-0347313P.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Wang T, Wang S, Bangur CS, Gaiger A;  
PI WPI; 2003-058387/05.  
XX  
DR New immunogenic polynucleotides or polypeptides useful for diagnosing,  
PT preventing and treating cancer expressing CT or CP mRNA antigens, and in  
PT virology, immunology, microbiology, molecular biology and recombinant DNA  
PT techniques.  
XX  
PS Claim 1; SEQ ID NO 2381; 207pp; English.  
XX

XX ABO17575 to ABO20506 represent isolated polynucleotide (I) sequences, and  
CC ABP5446 to ABP54472 represent protein (II) sequences, from the present  
CC invention. (I) and (II) have cytosstatic activity and can be used in gene  
CC therapy and vaccines. (I), (II), antibodies and compositions from the  
CC present invention are useful for diagnosing, preventing and treating  
CC cancer, which expresses CT or CP mRNA antigens. They are useful for  
CC stimulating immune response. They can also be useful in virology,  
CC immunology, microbiology, molecular biology and recombinant DNA  
CC techniques. N.B. The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 257 BP; 57 A; 74 C; 62 G; 64 T; 0 U; 0 Other;

Query Match 44.2%; Score 235.4; DB 7; Length 257;  
Best Local Similarity 99.6%; Pred. No. 4.6e-59;  
Matches 236; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AGCTGTGAGGCGAGTGTGTGTTCTCGCGTCCGGACTCTTTTCTCTACTGAGATT 60  
Db 237 AGCTGTGAGGCGAGTGTGTGTTCTCGCGTCCGGACTCTTTTCTCTACTGAGATT 178  
QY 61 CATCTGTGAAATATAGATTGGCGAGGAAGATCGACCTATTATTGCGCTTAGACCAAGGC 120  
Db 177 CATCTGTGAAATATAGATTGGCGAGGAAGATCGACCTATTATTGCGCTTAGACCAAGGC 118  
QY 121 GCTATGTACAGCTCTCTGAGTGATTGGGCTTATGCGGCCCGAGCAGTTCAGTGATGAAG 180  
Db 117 GCTATGTACAGCTCTCTGAGTGATTGGGCTTATGCGGCCCGAGCAGTTCAGTGATGAAG 58  
QY 181 TGGAAACAGCAACACCTTGAAAGAGGGGAACAGCAACTCAACGTCAGGATCCTGCAG 237  
Db 57 TGGAAACAGCAACACCTTGAAAGAGGGGAACAGCAACTCAACGTCAGGATCCTGCAG 1

RESULT 14  
ABZ19755  
ID ABZ19755 standard; cDNA; 264 BP.  
XX  
AC ABZ19755;  
XX  
DT 23-JAN-2003 (first entry)  
XX  
DE Group III cDNA cancer related clone SEQ ID NO:2181.  
XX  
KW Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;  
KW immune response; virology; immunology; microbiology; molecular biology;  
KW recombinant DNA technology; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200278516-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 28-MAR-2002; 2002WO-US010421.  
XX  
PR 30-MAR-2001; 2001US-0280255P.  
PR 28-AUG-2001; 2001US-0315563P.  
PR 09-JAN-2002; 2002US-0347313P.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
XX Wang T, Wang S, Bangur CS, Gaiger A;  
PI  
XX WPI; 2003-058387/05.  
XX  
DR

New immunogenic polynucleotides or polypeptides useful for diagnosing,  
PT preventing and treating cancer expressing CT or CP mRNA antigens, and in  
PT virology, immunology, microbiology, molecular biology and recombinant DNA  
PT techniques.

PS Claim 1; SEQ ID NO 2181; 207pp; English.  
XX  
CC ABO17575 to ABO20506 represent isolated polynucleotide (I) sequences, and  
CC ABP5446 to ABP54472 represent protein (II) sequences, from the present  
CC invention. (I) and (II) have cytosstatic activity and can be used in gene  
CC therapy and vaccines. (I), (II), antibodies and compositions from the  
CC present invention are useful for diagnosing, preventing and treating  
CC cancer, which expresses CT or CP mRNA antigens. They are useful for  
CC stimulating immune response. They can also be useful in virology,  
CC immunology, microbiology, molecular biology and recombinant DNA  
CC techniques. N.B. The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 264 BP; 64 A; 66 C; 75 G; 59 T; 0 U; 0 Other;

Query Match 44.2%; Score 235.4; DB 7; Length 264;  
Best Local Similarity 99.6%; Pred. No. 4.7e-58;  
Matches 236; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AGCTGTGAGGCGAGTGTGTGTTCTCGCGTCCGGACTCTTTTCTCTACTGAGATT 60  
Db 28 AGCTGTGAGGCGAGTGTGTGTTCTCGCGTCCGGACTCTTTTCTCTACTGAGATT 87  
QY 61 CATCTGTGAAATATAGATTGGCGAGGAAGATCGACCTATTATTGCGCTTAGACCAAGGC 120  
Db 88 CATCTGTGAAATATAGATTGGCGAGGAAGATCGACCTATTATTGCGCTTAGACCAAGGC 147  
QY 121 GCTATGTACAGCTCTCTGAGTGATTGGGCTTATGCGGCCCGAGCAGTTCAGTGATGAAG 180  
Db 148 GCTATGTACAGCTCTCTGAGTGATTGGGCTTATGCGGCCCGAGCAGTTCAGTGATGAAG 207  
QY 181 TGGAAACAGCAACACCTTGAAAGAGGGGAACAGCAACTCAACGTCAGGATCCTGCAG 237  
Db 208 TGGAAACAGCAACACCTTGAAAGAGGGGAACAGCAACTCAACGTCAGGATCCTGCAG 264

RESULT 15  
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ID ABZ20497 standard; cDNA; 229 BP.  
XX  
AC ABZ20497;  
XX  
DT 23-JAN-2003 (first entry)  
XX  
DE TP51 subtraction library cDNA clone SEQ ID NO:2950.  
XX  
KW Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;  
KW immune response; virology; immunology; microbiology; molecular biology;  
KW recombinant DNA technology; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200278516-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 28-MAR-2002; 2002WO-US010421.  
XX  
PR 30-MAR-2001; 2001US-0280255P.  
PR 28-AUG-2001; 2001US-0315563P.  
PR 09-JAN-2002; 2002US-0347313P.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
XX Wang T, Wang S, Bangur CS, Gaiger A;  
PI  
XX WPI; 2003-058387/05.  
XX  
DR

New immunogenic polynucleotides or polypeptides useful for diagnosing,  
PT preventing and treating cancer expressing CT or CP mRNA antigens, and in  
PT virology, immunology, microbiology, molecular biology and recombinant DNA  
PT techniques.

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XX
PS Claim 1; SEQ ID NO 2950; 207pp; English.
XX
CC ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and
CC ABP5446 to ABP54472 represent protein (II) sequences, from the present
CC invention. (I) and (II) have cytosolic activity and can be used in gene
CC therapy and vaccines. (I), (II), antibodies and compositions from the
CC present invention are useful for diagnosing, preventing and treating
CC cancer, which expresses CT or CP mRNA antigens. They are useful for
CC stimulating immune response. They can also be useful in virology,
CC immunology, microbiology, molecular biology and recombinant DNA
CC techniques. N.B. The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
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SQ Sequence 229 BP; 56 A; 55 C; 64 G; 54 T; 0 U; 0 Other;
  Query Match      42.7%; Score 227.4; DB 7; Length 229;
  Best Local Similarity 99.6%; Pred. No. 9.2e-56;
  Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 GGCAGTGTGTGTGTTCTCTGCGTCCGGACTCTTTTCTCTACTGAGATTCATCTGTG 60
QY 69 TGAATATGAGTTGGCGAGGAGATCGACTATTATTGGCTAGACCAAGCGCTATGTA 128
Db 61 TGAATATGAGTTGGCGAGGAGATCGACTATTATTGGCTAGACCAAGCGCTATGTA 120
QY 129 CAGCTTCTGAGTGTGTTGGGCTATGCGGCCGAGCAGTTCAAGTGAAGTGAACCA 188
Db 121 CAGCTTCTGAGTGTGTTGGGCTATGCGGCCGAGCAGTTCAAGTGAAGTGAACCA 180
QY 189 GCAACACCTGAGAGAGGGGAACCACTCAACGTCAGATCCTGCAG 237
Db 181 GCAACACCTGAGAGAGGGGAACCACTCAACGTCAGATCCTGCAG 229
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Job time : 335 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 19:34:25 ; Search time 374 Seconds  
(without alignments)  
3521.250 Million cell updates/sec

Title: US-09-782-745-17

Perfect score: 532

Sequence: 1 AGCTGTGAGGCGAGTGTGTG.....CTCCAAAGAAAAA 532

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4761877 seqs, 1237732561 residues

Total number of hits satisfying chosen parameters: 8521116

Minimum DB seq length: 0

Maximum DB seq length: 532

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_NA\_New:

- 1: /cgn2\_6/prodata/1/pna/PCT\_NEW\_COMB.seq.\*
- 2: /cgn2\_6/prodata/1/pna/US06\_NEW\_COMB.seq.\*
- 3: /cgn2\_6/prodata/1/pna/US07\_NEW\_COMB.seq.\*
- 4: /cgn2\_6/prodata/1/pna/US08\_NEW\_COMB.seq.\*
- 5: /cgn2\_6/prodata/1/pna/US09\_NEW\_COMB.seq.\*
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- 8: /cgn2\_6/prodata/1/pna/US10\_NEW\_COMB.seq.\*
- 9: /cgn2\_6/prodata/1/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517.4	97.3	528	7	US-10-782-413-16
2	350.8	65.9	430	7	US-10-793-479-2127
3	208.4	39.2	520	8	US-10-473-603-38
4	140.0	26.3	528	8	US-10-473-603-20
5	137.8	25.9	336	7	US-10-821-234-695
6	133.2	25.0	475	5	US-09-970-607-3
7	133.2	25.0	475	5	US-10-453-372-485
8	128.6	24.2	336	7	US-10-821-234-590
9	118.8	22.3	501	7	US-10-453-372-475
10	118	22.2	448	5	US-09-970-607-44
11	111.6	21.0	448	5	US-09-970-607-43
12	101.6	19.1	515	5	US-09-570-737A-472
13	99.8	18.8	374	7	US-10-453-372-477
14	97.4	18.3	337	7	US-10-453-372-479
15	96.4	18.1	344	7	US-10-453-372-487
16	94.8	17.8	343	7	US-10-453-372-483
17	94.8	17.8	343	7	US-10-453-372-481
18	86.4	16.2	348	5	US-09-970-607-109
19	85.4	16.1	336	7	US-10-453-372-473
20	85.2	16.0	499	1	PCT-US02-22858A-684
21	82.8	15.6	458	7	US-10-453-372-469
22	81.2	15.3	458	5	US-09-970-607-1
23	81.2	15.3	458	7	US-10-453-372-471
24	80.8	15.2	309	7	US-10-821-234-605
					Sequence 16, Appl
					Sequence 2127, Ap
					Sequence 38, Appl
					Sequence 20, Appl
					Sequence 695, App
					Sequence 3, Appli
					Sequence 485, App
					Sequence 590, App
					Sequence 475, App
					Sequence 44, Appl
					Sequence 43, Appl
					Sequence 472, App
					Sequence 477, App
					Sequence 479, App
					Sequence 487, App
					Sequence 483, App
					Sequence 481, App
					Sequence 109, App
					Sequence 473, App
					Sequence 684, App
					Sequence 469, App
					Sequence 1, Appli
					Sequence 471, App
					Sequence 605, App

25	78.6	14.8	334	8	US-10-473-603-46	Sequence 46, Appl
26	57	10.7	69	7	US-10-834-268-3287	Sequence 3287, Ap
27	53	10.0	157	7	US-10-793-479-19668	Sequence 19668, A
28	51	9.6	51	8	US-10-865-478-612	Sequence 612, App
29	49.4	9.3	51	8	US-10-865-478-421	Sequence 421, App
30	49.4	9.3	51	8	US-10-865-478-613	Sequence 613, App
31	48.8	9.2	110	5	US-09-970-607-31	Sequence 31, Appl
32	48.2	9.1	122	5	US-09-970-607-36	Sequence 36, Appl
33	45.6	8.6	110	5	US-09-970-607-32	Sequence 32, Appl
34	43.6	8.2	114	5	US-09-970-607-140	Sequence 140, App
35	41.6	7.8	472	7	US-10-674-124A-5858	Sequence 5858, Ap
36	40.2	7.6	119	5	US-09-970-607-33	Sequence 33, Appl
37	39.6	7.4	415	6	US-10-425-115-51014	Sequence 51014, A
38	39	7.3	395	1	PCT-US04-07668-45	Sequence 45, Appl
39	38.6	7.3	119	5	US-09-970-607-34	Sequence 34, Appl
40	36.6	6.9	387	7	US-10-674-124A-15877	Sequence 15877, A
41	36	6.8	493	6	US-10-501-933-1267	Sequence 1267, Ap
42	36	6.8	493	9	US-60-554-981-523	Sequence 523, App
43	36	6.8	493	9	US-60-559-949-207	Sequence 207, App
44	35.4	6.7	356	5	US-09-404-520B-27194	Sequence 27194, A
45	35.2	6.6	498	6	US-10-425-115-149178	Sequence 149178, A

#### ALIGNMENTS

##### RESULT 1

US-10-782-413-16  
; Sequence 16, Application US/10782413  
; GENERAL INFORMATION:  
; APPLICANT: Ortho-Clinical Diagnostics, Inc.  
; APPLICANT: Wang, Yixin  
; TITLE OF INVENTION: Colorectal Cancer Prognostics  
; FILE REFERENCE: VDX-5002 CIP  
; CURRENT APPLICATION NUMBER: US/10/782,413  
; CURRENT FILING DATE: 2004-02-18  
; PRIOR APPLICATION NUMBER: 10/651,237  
; PRIOR FILING DATE: 2003-08-28  
; NUMBER OF SEQ ID NOS: 94  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 16  
; LENGTH: 528  
; TYPE: DNA  
; ORGANISM: human  
US-10-782-413-16

Query Match		97.3%	Score 517.4;	DB 7;	Length 528;
Best Local Similarity		99.8%	Pred. No. 1.7e-149;		
Matches 518;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	AGCTGTGAGGCGAGTGTGTGTCTCTCCCGTCCGAGCTCTTTTCTCTACTGAGATT	60		
Db	9	AGCTGTGAGGCGAGTGTGTGTCTCTCCCGTCCGAGCTCTTTTCTCTACTGAGATT	68		
QY	61	CATCTGTGTGAATATGACTTGGCGAGGAGATCGACCTATTATGGCCCTAGCCOMAGGC	120		
Db	69	CATCTGTGTGAATATGACTTGGCGAGGAGATCGACCTATTATTTGGCCCTAGACCAAGGC	128		
QY	121	GCTATGTACAGCTCTCTGAAGTATTGGCCCTATGCGCCCGAGCAGTTCAGTGATGAG	180		
Db	129	GCTATGTACAGCTCTCTGAATATTGGCCCTATGCGCCCGAGCAGTTCAGTGATGAG	188		
QY	181	TGGAAACAGCAACCTGAAGAAGGGGAACCAAGCACTCAAGCTCAGGATCTTCGAGCTG	240		
Db	189	TGGAAACAGCAACCTGAAGAAGGGGAACCAAGCACTCAAGCTCAGGATCTTCGAGCTG	248		
QY	241	CTCAGAGGAGAGATGAGGAGCATCTGAGGTCAGGGCCGAAGCCTCAAGCTGATA	300		
Db	249	CTCAGAGGAGAGATGAGGAGCATCTGAGGTCAGGGCCGAAGCCTCAAGCTGATA	308		
QY	301	GCCAGGAACAGGCTCACCCACAGCTGGGTGTGAGTGTGAACATGCTCTGATGGCAGG	360		
Db	309	GCCAGGAACAGGCTCACCCACAGCTGGGTGTGAGTGTGAACATGCTCTGATGGCAGG	368		

QY 361 AGATGACCGCCAAATCCAGAGAGTGAAGCGCTGAAGAGGTGAAGCAATCAC 420  
Db 369 AGATGACCGCCAAATCCAGAGAGTGAAGCGCTGAAGAGGTGAAGCAATCAC 428  
QY 421 AGTGTAAAGAGGACGCTTGAATGATGAGGCTGCTCTATGTTGGAAATTTGTCA 480  
Db 429 AGTGTAAAGAGGACGCTTGAATGATGAGGCTGCTCTATGTTGGAAATTTGTCA 488  
QY 481 TTAATAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAA 519  
Db 489 TTAATAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAA 527

## RESULT 2

US-10-793-479-2127  
; Sequence 2127, Application US/10793479  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/10/793,479  
; CURRENT FILING DATE: 2004-03-03  
; PRIOR APPLICATION NUMBER: US/09/513,999  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681

; SOFTWARE: Patent.pm

; SEQ ID NO 2127

; LENGTH: 430

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 202...429

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: 31

; OTHER INFORMATION: n=a, g, c or t

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: 32

; OTHER INFORMATION: k=g or t

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: 164

; OTHER INFORMATION: n=a, g, c or t

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: 166

; OTHER INFORMATION: y=c or t

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: 180

; OTHER INFORMATION: r=a or g

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: 283

; OTHER INFORMATION: y=c or t

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: 307

; OTHER INFORMATION: r=a or g

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: 429

; OTHER INFORMATION: m=a or c

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: 28

; OTHER INFORMATION: Xaa=Cys or Arg

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: 36

; OTHER INFORMATION: Xaa=Glu or Lys

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: 76

; OTHER INFORMATION: Xaa=Asp or Glu

; US-10-793-479-2127

Query Match 65.9%; Score 350.8; DB 7; Length 430;

Best Local Similarity 97.6%; Pred. No. 4.9e-98;

Matches 360; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

QY 1 AGCTGTGAGGAGTGTGTGTTCTGCGCTCCGACTCTTTTCTCTACTGAGATT 60  
Db 63 AGCTGTGAGGAGTGTGTGTTCTGCGCTCCGACTCTTTTCTCTACTGAGATT 122  
QY 61 CATCTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGC 120  
Db 123 CATCTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATNA-YGGCCTAGACCAAGRC 181  
QY 121 GCTATGTACAGCTCTCTGAAAGTGTGGGCTATGCGGCCGAGCAGTTCAGTGTGAAG 180  
Db 182 GCTATGTACAGCTCTCTGAAATGATTTGGGCTATGCGGCCGAGCAGTTCAGTGTGAAG 241  
QY 181 TGGAAACAGCAACACCTGGAAGAGGGGAACCCAGCAACTCAACGTGAGGATCTGCAGCTG 240  
Db 242 TGGAAACAGCAACACCTGGAAGAGGGGAACCCAGCAACTCAAYGTGAGGATCTGCAGCTG 301  
QY 241 CTCAGGAGGAGAGGATGAGGAGCATCTGCAGGTCAAGGCCGAGGCTGAAGTGTATA 300  
Db 302 CTCAGGAGGAGAGGATGAGGAGCATCTGCAGGTCAAGGCCGAGGCTGAAGTGTATA 361  
QY 301 GCCAGGAACAGGTCACCCACAGACTGGTGTGAGTGTGAGAGTGTCTCTGATGGCAGG 360  
Db 362 GCCAGGAACAGGTCACCCACAGACTGGTGTGAGTGTGAGAGTGTCTCTGATGGCAGG 421  
QY 361 AGATGGACC 369  
Db 422 AGATGGACC 430

## RESULT 3

US-10-473-603-38  
; Sequence 38, Application US/10473603  
; GENERAL INFORMATION:  
; APPLICANT: OLD, Lloyd  
; APPLICANT: SCANLAN, Matthew  
; APPLICANT: CHEN, Yao-Tseung  
; TITLE OF INVENTION: CANCER-TESTIS ANTIGENS  
; FILE REFERENCE: I0461.70155US00  
; CURRENT APPLICATION NUMBER: US/10/473,603  
; CURRENT FILING DATE: 2003-09-30  
; PRIOR APPLICATION NUMBER: PCT/US02/09808  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: 10/054,683  
; PRIOR FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: 60/280,718  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 60/285,154  
; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: 60/327,432  
; PRIOR FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 38  
; TYPE: DNA  
; LENGTH: 520  
; ORGANISM: Homo sapiens  
; US-10-473-603-38



Db 100 CCTCAGCAAGAGAACCCACCACTGAAGTCGGATCCTGCACCTGTGTCAGAGAGAA 159  
QY 252 GAGGATGAGGAGCATCTGCAGGTCAAGGCCGAAAGCCTGAAGCTGATGATCCAGGAAAG 311  
Db 160 GAAGATCAGGCTGCAGCTGAGACTCAAGTGCCTGACCTGGAAGCTGATCTCCAGGAGCTG 219  
QY 312 GGTCAACCCAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGGACAGAGATGGACCG 371  
Db 220 TCTCAGTCAAGAGACTGGGGGTGAATGTGGAATGGTCTGATGACCAAGGGAAGATTCGT 279  
QY 372 CCAAAATCCAGAGAGGTGAAACCCCTGAAAGAGGTGAAAGCAATCACAAGTGTAA 428  
Db 280 CCAAAATCAGACAACTTAAATGCCAGAGAGAGTGCACGGCAACCAAGGTTAA 336

## RESULT 6

US-09-970-607-3  
; Sequence 3, Application US/09970607  
; GENERAL INFORMATION:  
; APPLICANT: Malyankar et al.  
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same  
; FILE REFERENCE: 15966-675 CIP2  
; CURRENT APPLICATION NUMBER: US/09/970,607  
; CURRENT FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: 60/182,733  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 60/182,724  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 60/183,896  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: 60/184,497  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/224,157  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/184,482  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,744  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/197,083  
; PRIOR FILING DATE: 2000-04-13  
; PRIOR APPLICATION NUMBER: 60/233,405  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: 60/236,060  
; PRIOR FILING DATE: 2000-09-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 475  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-970-607-3

Query Match 25.0%; Score 133.2; DB 5; Length 475;  
Best Local Similarity 59.8%; Pred. No. 9.6e-31;  
Matches 286; Conservative 0; Mismatches 173; Indels 19; Gaps 3;

QY 61 CATCTGTGGAATATGAGTTGGCGAGGAAGTGCACCTATTATTGGCCCTAGACCAAGC 120  
Db 11 CATGTGTGGAATATGAGTGCAGCATGTGAGAACAAAGATCCCAATCCTCAGAAAGAGAA 70  
QY 121 GCTATGTACAGCTCTGAGTGTGGCCCTATCGGCCCGAGAGTTCAGTGATGAAG 180  
Db 71 ATGACCAAGAGTCTTCCCAAGCAGTGTGATCTGATGTTCCAGAGCCCATGAGGA-- 128  
QY 181 TGAACACCAAGCAACCTGAAAGAGGGGAAACCAAGCAACTCAACGTGAGGATCCTGAGCTG 240  
Db 129 -----AAAACGTCAAGAGGAAGAACCAACCAACTGATAATCAGGGTATTGCACCTA 178  
QY 241 CTCAGAGGAGAGGATGAGGAGCATCTGAGTCAAGGCCGGAAGCCCTGAGCTGATA 300  
Db 179 GTGGGAGATCGAAATGAAGGAGCACCTGCCCTTCAAGGGCCCTGATGGAAGCTTTTC 238

QY 301 GCAGGAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGTCCTGATGGGAGG 360  
Db 239 AACAGGAACCTGGCTCTGCTTAAGATAGAGATGAGCTGGAGATGCTCTGATGTCAGGG 298  
QY 361 AGATGGAACCCGCGCAAAATCCAGAGGAGGTGAAACGCTTGAAGAGGTGAAAGCAATCAC 420  
Db 299 AGGGGATTAATGCCCCACTTTTGTGATCTCACTAAAGTGTGGAAGCAGGTGATGCGCAACCAT 358  
QY 421 AGTGTAAAAGAGGACCGT-----TGAATGATGAGGCTGCTCCTATGTTGGAAT 474  
Db 359 AGTGTCAAGCAAGACAAATGAAGACTGAAACCCAGAACGTTATTCTTAATCTGGAAT 418  
QY 475 TGTTCAATTAATAATTCCTCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA 532  
Db 419 TGACTGATAATATCTCTTAATAAGTTTAA-AGTTTCTGCAAGAAAAA 475

## RESULT 7

US-10-453-372-485  
; Sequence 485, Application US/10453372  
; GENERAL INFORMATION:  
; APPLICANT: Alsbrook, et al.  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-589 A  
; CURRENT APPLICATION NUMBER: US/10/453,372  
; CURRENT FILING DATE: 2003-06-03  
; PRIOR APPLICATION NUMBER: 09/789390  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 60/185967  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: 09/823187  
; PRIOR FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 60/195792  
; PRIOR FILING DATE: 2000-03-10  
; PRIOR APPLICATION NUMBER: 09/839446  
; PRIOR FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: 60/199476  
; PRIOR FILING DATE: 2000-03-25  
; PRIOR APPLICATION NUMBER: 09/863776  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: 60/208263  
; PRIOR FILING DATE: 2000-05-31  
; PRIOR APPLICATION NUMBER: 09/939398  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 60/227800  
; PRIOR FILING DATE: 2000-08-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1609  
; SOFTWARE: Curaseqdist version 0.1  
; SEQ ID NO 485  
; LENGTH: 475  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(357)  
US-10-453-372-485

Query Match 25.0%; Score 133.2; DB 7; Length 475;  
Best Local Similarity 59.8%; Pred. No. 9.6e-31;  
Matches 286; Conservative 0; Mismatches 173; Indels 19; Gaps 3;

QY 61 CATCTGTGGAATATGAGTTGGCGAGGAAGTGCACCTATTATTGGCCCTAGACCAAGC 120  
Db 11 CATGTGTGGAATATGAGTGCAGCATGTGAGAACAAAGATCCCAATCCTCAGAAAGAGAA 70  
QY 121 GCTATGTACAGCTCTGAGTGTGGCCCTATCGGCCCGAGAGTTCAGTGATGAAG 180  
Db 71 ATGACCAAGAGTCTTCCCAAGCAGTGTGATCTGATGTTCCAGAGCCCATGAGGA-- 128  
QY 181 TGAACACCAAGCAACCTGAAAGAGGGGAAACCAAGCAACTCAACGTGAGGATCCTGAGCTG 240



Db 129 -----AAAACGTCAAGAGAGGAAACCAACCACTGATAATACAGGGTATTGCACCTA 178  
 QY 241 CTCAGGAGGAGAGGATGAGGAGCATCTGCAGGTCAAGGCCCAAGCCTGAAGCTGATA 300  
 Db 179 GTGGGAGATCGAAATGAAGGACACCTGCCGTCAAGGCCCTGACATGGAAGCTTTTC 238  
 QY 301 GCCAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTTATGATGGCAGG 360  
 Db 239 AACAGGAACCTGGTCTCTCTTAAGATAGAGGTGAGCTGGAGATGGTCTTATGATCGAGG 298  
 QY 361 AGATGGACCCGCAAAATCCAGAGAGGTGAAAGCGCTGAAGAGGTGAAAGCAATCAC 420  
 Db 299 AGGGGATATGCCACCTTTTGTATCTCACTAAAGTGTGGAAGCAGGTGATGCGCAACCAT 358  
 QY 421 AGTGTAAAGAACGACGT-----TGAATGATGAGGCTGCTCTATGTTGGAAATT 474  
 Db 359 AGGTTCAAGCAAGACAAATGAAGACTGAAACCAAGAACCTTATCTTAATCTGGAATT 418  
 QY 475 TGTTCATTAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAAAGAAAAA 532  
 Db 419 TGACTGATAATATCTCTTAATAAAGTTTAA-AGTTTCTGCAAGAAAAAAGAAAAA 475

## RESULT 8

US-10-821-234-590  
 ; Sequence 590, Application US/10821234  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Labat, Ivan  
 ; APPLICANT: Stache-Crain, Birgit  
 ; APPLICANT: Andarmani, Susan  
 ; APPLICANT: Tang, Y. Tom  
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
 ; FILE REFERENCE: 821A  
 ; CURRENT APPLICATION NUMBER: US/10/821,234  
 ; PRIOR FILING DATE: 2004-04-07  
 ; PRIOR APPLICATION NUMBER: US 60/462,047  
 ; NUMBER OF SEQ ID NOS: 1704  
 ; SOFTWARE: pt\_seq\_genes Version 1.0  
 ; SEQ ID NO 590  
 ; LENGTH: 336  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-821-234-590

Query Match 24.2%; Score 128.6; DB 7; Length 336;  
 Best Local Similarity 66.9%; Pred. No. 2.1e-29;  
 Matches 239; Conservative 0; Mismatches 94; Indels 24; Gaps 3;  
 QY 75 ATGAGTTGCGAGGAGATCGACCTATTATTGGCCTTAGACCAAGGCGCTATCTACAGCCT 134  
 Db 1 ATGAGTTGCGAGGAGATCAAC---ATATAGCCTTAGCCCAAGAGAGTTTACAGCCT 57  
 QY 135 CTGAGTGTATGGGCTTATGCGGCCGAGCAGTTTCAAGTATGAAGTGAACCAACA 194  
 Db 58 CTGAGCTGATTTGGGCTATGCT-----TGAACCCACTGATGAAG 99  
 QY 195 CTGAAGAGGAGGAGACCAAGCACTCAAGCTCAGATCTCTGAGCTCTCAGAGGAGAG 254  
 Db 100 CTTAAGAGAGAAACCCCACTAAAGTGGAAATCTACACCTGATCAGAAGAGAGAA 159  
 QY 255 GATG---AGGAGCATCTGCAGGTCAAGGCCCGAAGCCTGAAGCTGATAGCCAGGAACAG 311  
 Db 160 GATGATCAGGTGTCAGCTGAGATTCAAGTGTCTGACCTGGAAGCCGATCTCAGAGCTA 219  
 QY 312 GGTACCCACAGATGGGTGTGAGTGTGAAGATGCTCTCTGATGGCAGGAGATGACCCG 371  
 Db 220 TGTACAGAAAGACTGGGGATGATGTGAAGTGTGTACTGATGTCAAGGGAGATTCTTA 279  
 QY 372 CCAATCCAGAGGAGGTGAAGCGCTCAAGAGGTGAAGAGCAATCAAGTGTAA 428  
 Db 280 CCAAGCAGAGCATTTTAAATATGCCAAGCAGGTGAAGGAGAAATCAAGGTTTAA 336

## RESULT 9

US-10-453-372-475  
 ; Sequence 475, Application US/10453372  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alsobrook, et al.  
 ; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
 ; FILE REFERENCE: 21402-589 A  
 ; CURRENT APPLICATION NUMBER: US/10/453,372  
 ; CURRENT FILING DATE: 2003-06-03  
 ; PRIOR APPLICATION NUMBER: 09/789390  
 ; PRIOR FILING DATE: 2001-02-23  
 ; PRIOR APPLICATION NUMBER: 60/185967  
 ; PRIOR FILING DATE: 2000-03-01  
 ; PRIOR APPLICATION NUMBER: 09/823187  
 ; PRIOR FILING DATE: 2001-03-29  
 ; PRIOR APPLICATION NUMBER: 60/195792  
 ; PRIOR FILING DATE: 2000-03-10  
 ; PRIOR APPLICATION NUMBER: 09/839446  
 ; PRIOR FILING DATE: 2001-03-19  
 ; PRIOR APPLICATION NUMBER: 60/199476  
 ; PRIOR FILING DATE: 2000-03-25  
 ; PRIOR APPLICATION NUMBER: 09/863776  
 ; PRIOR FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: 60/208263  
 ; PRIOR FILING DATE: 2000-05-31  
 ; PRIOR APPLICATION NUMBER: 09/939398  
 ; PRIOR FILING DATE: 2001-08-24  
 ; PRIOR APPLICATION NUMBER: 60/227800  
 ; PRIOR FILING DATE: 2000-08-25  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 1609  
 ; SOFTWARE: CuraSeqList version 0.1  
 ; SEQ ID NO 475  
 ; LENGTH: 501  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (25)..(357)  
 US-10-453-372-475

Query Match 22.3%; Score 118.8; DB 7; Length 501;  
 Best Local Similarity 57.9%; Pred. No. 2.8e-26;  
 Matches 277; Conservative 0; Mismatches 182; Indels 19; Gaps 3;  
 QY 61 CATCTGTGTGAATATGATGTTGGCAGGAAGATCCACCTATTATTGGCTAGACCAAGC 120  
 Db 11 CATGTGTGGGAATATGATGAGCTTTGTAAGAACCAAGATCCCAATCCTCAGAAAGAGAA 70  
 QY 121 GCTATGTACAGCTCTCTGAAGTGAATTGGGCTTATCGGCCCGAGCAGTTCAGTGATGAAG 180  
 Db 71 ATGACCAAGAGTCTCCACAGCCGTTGATCTGTGATGTTCAGGAGCCCTAGAGGA-- 128  
 QY 181 TGAACACGACACCTGAAGAGGGAAACAGCAACTCAACGTTCAGGATCTCGAGCTG 240  
 Db 129 -----AAAACGTCAAGAGAGGAAACCAACCACTGATAATCAGGSTATTCACCTA 178  
 QY 241 CTCAGGAGGAGAGATGAGGAGCATCTGCAGGTCAAGGCCCGAAGCCTGAAGCTGATA 300  
 Db 179 GTGGGAGATTGAAATCAAGCAGTGCCTTTTTCAGGGCCCTGCATGGAAGCTTTTC 238  
 QY 301 GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGCAGG 360  
 Db 239 AACAGGAACCTGGCTCTCTTAAAGATAGAGATGAGCCTTGGAGATGGTCTCTGATGTGAGG 298  
 QY 361 AGATGGACCCGCAAAATCCAGAGAGGTGAAACCGCTTGAAGAGGTGAAAGCAATCAC 420  
 Db 299 AGGGTATTATGCCACCTTTTGTATCTCACTAAAGTGTGGAAGCAGGTGATCGGCAACCAT 358  
 QY 421 AGTCTTAAAGAGGACAGT-----TGAATGATGAGGCTGCTCTTATGTTCGAAATT 474  
 Db 359 AGGTTTCAAGCAAGACAAATGAAGACTGAAACCAAGAACGTTATTCTTAATCTGGAATT 418

Db 349 TCAAGCAGACAAATCCCAATTAAGCTGAAACCAAGAACGTTATTCTTAATCTCGAAATTTGACT 408  
QY 480 ATTAAATTTCTCCCAATAAAGCTTTA 505  
Db 409 GATATATTTCTCTTAATAAAGTTTA 434

RESULT 11

US-09-970-607-43  
; Sequence 43, Application US/09970607  
; GENERAL INFORMATION:  
; APPLICANT: Malyankar et al.  
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same  
; FILE REFERENCE: 15966-675 CIP2  
; CURRENT APPLICATION NUMBER: US/09/970,607  
; CURRENT FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: 60/182,733  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 60/182,724  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 60/183,896  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: 60/184,497  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/224,157  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/184,482  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,744  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/197,083  
; PRIOR FILING DATE: 2000-04-13  
; PRIOR APPLICATION NUMBER: 60/233,405  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: 60/236,060  
; PRIOR FILING DATE: 2000-09-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 43  
; LENGTH: 448  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-970-607-43

Query Match 21.0%; Score 111.6; DB 5; Length 448;  
Best Local Similarity 57.0%; Pred. No. 4.4e-24;  
Matches 254; Conservative 0; Mismatches 174; Indels 18; Gaps 2;  
QY 66 GTGTGAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGCGCTAT 125  
Db 1 GTGGGAATATGAGTGAGCTTTGTAAGAGCAAGATCCCAATCCTCAGAAAGAGGAATGAC 60  
QY 126 GTACAGCTCTTGAAGTGAATTTGGGCTATGGCCGAGAGCTTCAGTGATCAAGTGAA 185  
Db 61 CAAGAGTCTTCCCGAGCGGTGGATCTGTGATTTCCAGGAGCCCACTGAGGA----- 113  
QY 186 CCAGCAACACCTGAAGAAGGGGAAACAGCAACTCAACCTCAGGATTCCTCAGCTGCTCAG 245  
Db 114 -----AAACGCTCAAGAGAGGAAACCAACTGATATCAGGATTTGCACCTAGTGGG 168  
QY 246 GAGGAGAGGATGAGGGAGCATCTCAGGTCAAGGGCCGAGCCTGAAGCTGATAGCCAG 305  
Db 169 GAGATCGAAATGAAGGACCACTGCCGTTCAAGGSCCTGACATGGAAGCTTTTCAACAG 228  
QY 306 GAACAGGGTCAACCAAGAGCTGGGTGTGAGTGTGAAGATGGTCTGATGGGAGGAGATG 365  
Db 229 GAACCTGGCTCTCTTAAAGATAGAGGATGAGCCTGGAGATGGTCTGATCTCAGGAGGGT 288  
QY 366 GACCCGCCAAATCCAGAGGAGGTGAAACGCTTGAAGAAGGTGAAAGCAATCACAAGTGT 425  
Db 289 ATTATGCCCACTTTTGTATCTCACTAAAGTGTGGAAGCAGGTGATCGCAACCATAGGTT 348

QY 475 TGTTCATTAATTTCTCCCAATTAAGCTTTAGAGCTTCTGCAAGCAAAAAA 532  
Db 419 TGACTGATAATATTTCTTTAATAAAGTTTA-AGTTTCTGCAAGAAATCTCAAAA 475

RESULT 10

US-09-970-607-44  
; Sequence 44, Application US/09970607  
; GENERAL INFORMATION:  
; APPLICANT: Malyankar et al.  
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same  
; FILE REFERENCE: 15966-675 CIP2  
; CURRENT APPLICATION NUMBER: US/09/970,607  
; CURRENT FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: 60/182,733  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 60/182,724  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 60/183,896  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: 60/184,497  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/224,157  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/184,482  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,744  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/197,083  
; PRIOR FILING DATE: 2000-04-13  
; PRIOR APPLICATION NUMBER: 60/233,405  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: 60/236,060  
; PRIOR FILING DATE: 2000-09-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 44  
; LENGTH: 448  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-970-607-44

Query Match 22.2%; Score 118; DB 5; Length 448;  
Best Local Similarity 57.8%; Pred. No. 4.6e-26;  
Matches 258; Conservative 0; Mismatches 170; Indels 18; Gaps 2;  
QY 66 GTGTGAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGCGCTAT 125  
Db 1 GTGGGAATATGAGTGAGCTTTGTAAGAGCAAGATCCCAATCCTCAGAAAGAGGAATGAC 60  
QY 126 GTACAGCTCTTGAAGTGAATTTGGGCTATGGCCGAGAGCTTCAGTGATCAAGTGAA 185  
Db 61 CAAGAGTCTTCCCGAGCGGTGGATCTGTGATTTCCAGGAGCCCACTGAGGA----- 113  
QY 186 CCAGCAACACCTGAAGAAGGGGAAACAGCAACTCAACCTCAGGATTCCTCAGCTGCTCAG 245  
Db 114 -----AAACGCTCAAGAGAGGAAACCAACTGATATCAGGATTTGCACCTAGTGGG 168  
QY 246 GAGGAGAGGATGAGGGAGCATCTCAGGTCAAGGGCCGAGCCTGAAGCTGATAGCCAG 305  
Db 169 GAGATCGAAATGAAGGACCACTGCCGTTCAAGGSCCTGACATGGAAGCTTTTCAACAG 228  
QY 306 GAACAGGGTCAACCAAGAGCTGGGTGTGAGTGTGAAGATGGTCTGATGGGAGGAGATG 365  
Db 229 GAACCTGGCTCTCTTAAAGATAGAGGATGAGCCTGGAGATGGTCTGATCTCAGGAGGGG 288  
QY 366 GACCCGCCAAATCCAGAGGAGGTGAAACGCTTGAAGAAGGTGAAAGCAATCACAAGTGT 425  
Db 289 ATTATGCCCACTTTTGTATCTCACTAAAGTGTGGAAGCAGGTGATCGCAACCATAGGTT 348  
QY 426 TAAAGAGAGGCACGT-----TGAAATGATGACAGGCTGCTCTTATGTTGGAATTTGTTTC 479

Qy	426	TAAAGAGCGCGT-----TGAATGATCGAGCTGCTCTATGTTGAAAATTTGTTTC	479
Db	349	TCAGCAAGACAAATTAAGACGTGAACACCAAGACGTTATTCTTAATCTGAAAATTTGACT	408
Qy	480	ATTAAATTCCTCCCAATAAGCTTTA	505
Db	409	GATAATATTCTCTTAATAAGTTTTA	434

RESULT 12

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US-09-570-737A-472
; Sequence 472, Application US/09570737A
; GENERAL INFORMATION:
;
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Helber, William

```

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;      ; REFERENCE: WILLIAM  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C14
```

; CURRENT APPLICATION NUMBER: US/09/570,737A  
 ; CURRENT FILING DATE: 2009-05-12

/ CURRENT FILING DATE: 2000-05-12  
 ; PRIOR APPLICATION NUMBER: 09/568,100

; PRIOR FILING DATE: 2000-05-09  
; PRIOR APPLICATION NUMBER: 09/536 857

PRIOR FILING DATE: 2000-03-27

; PRIOR APPLICATION NUMBER: 09/483,672  
; PRIOR FILING DATE: 2000-01-14

; PRIOR APPLICATION NUMBER: 09/443,686

EXPIRATION DATE: 1999-11-18  
PRIOR APPLICATION NUMBER: 09/439,313

; PRIOR FILING DATE: 1999-11-12  
: PRIOR APPLICATION NUMBER: 09/352 516

PRIOR FILING DATE: 1999-07-13

;; PRIOR APPLICATION NUMBER: 09/288,946  
;; PRIOR FILING DATE: 1999-04-09

PRIOR APPLICATION NUMBER: 09/232,149

/ PRIOR FILING DATE: 1999-01-15  
 / PRIOR APPLICATION NUMBER: 09-159,812  
 / PRIOR FILING DATE: 1998-09-23  
 / PRIOR APPLICATION NUMBER: 09/115,453  
 / PRIOR FILING DATE: 1998-07-14  
 / Remaining Prior Application data removed - See File Wrapper or PALM

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; NUMBER OF SEQ ID NOS: 780
; SOFTWARE: FastSEQ for Windows Version 3.0

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; SEQ ID NO 472
; LENGTH: 515
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(515)
; OTHER INFORMATION: n = A,T,C or G
US-09-570-737A-472

```

Db	141	TGCAGCCCGGTGAATCTCTAGCAGAGAGAACCCACCAATCTGCAATCAGGATATTGAAACCTG	200
Qy	241	CTCAGAGGGAGAGATGAGGGAGCATCTGCAGGTCTCAAGGGCCGAAGCCCTGAAGCTGATA	300
Db	201	GACAAGAGAGAGAA-----GGAAACACCTCCGATCGAAGAACGTAAGGTAGAAGGTGATT	254
Qy	301	GCCAGGAACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGTGATGGGCAGG	360
Db	255	GCCAGGAATGGATCTGGAAGAAGACTCGAGGTGAGCGGTGGAGATGGCTCTGTGATGAAAAAG	314
Qy	361	AGATGGACCCGCCAAATCCAGAGGAGGTGAAACGCCCTGAAGAAGTGAAGACCAATCAC	420
Db	315	AGAAGACTCCACCTTAATCCTTAAGCATGTAAAGACTAAGAAGCAGAGATGGCAGCCAT	374
Qy	421	AGTGTATAAAGAAGCAGCTTTGAATGATGCA---GGTGTCTCTATGTTGGAAATTTG-	476
Db	375	AAGTTAAAGAAGAACAAGCTGAAGCTACACATGGCTGATGTCCATTTGAATAATGCA	434
Qy	477	-----TTCATTAAAAATTCCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA	531
Db	435	CTGAATAATTGAAAAATTCATATAAAGTTTGAGTTTCTCTGAAGAAAAAANA	494
Qy	532	A 532	
Db	495	A 495	

## RESULT 13

US-10-453-372-477

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; sequence 477, Application
; GENERAL INFORMATION:

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; APPLICANT: Alsbrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTI
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372

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; CURRENT FILING DATE: 2003-06-03  
: PRIOR APPLICATION NUMBER: 00/780200

; PRIORITY FILING DATE: 2001-02-23

; PRIOR APPLICATION NUMBER: 60/185967  
; PRIOR FILING DATE: 2000-03-01

;; PRIOR APPLICATION NUMBER: 09/823187

;; PRIOR FILING DATE: 2001-03-29  
;; PRIOR APPLICATION NUMBER: 60/195792

; PRIOR FILING DATE: 2000-03-10

;  
;  
; PRIOR FILING DATE: 2001-03-19

; PRIOR APPLICATION NUMBER: 60/199476  
: PRIOR FILING DATE: 2000-03-25

FILED DATE: 2000-03-23  
PRIOR APPLICATION NUMBER: 09/863776

; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: 60/208263

FILED: 00/200203  
; PRIOR FILING DATE: 2000-05-31

;; PRIOR APPLICATION NUMBER: 09/9393  
;; PRIOR FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: 60/2278

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; FILE FILLING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper 0
;
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 477
; LENGTH: 374
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (23)..(355)
US-10-453-372-477

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Db 231 CTGGCTCTGCTTAAGATAGAGGATGAGCCTGGAGATGGTCCTGATGTCAGGAGGGGATT 290  
Qy 369 CCGCCAAATCCAGAGGAGGTGAATAACGGCTGAAGAAGGTGAAAGCAATCAG 422  
Db 291 ATGCCCACTTTTGATCTCACTAAGTGTGGAAGCAGGTGATGCCACCATAG 344

Search completed: August 6, 2004, 21:54:17  
Job time : 375 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2004, 11:07:15 ; Search time 3602 Seconds  
(without alignments)  
6485.812 Million cell updates/sec

Title: US-09-782-745-18  
Perfect score: 539  
Sequence: 1 GCCAGGAGCTGTGAGGAC.....CTGCAAAAAAAAAAAAAA 539

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 3985670

Minimum DB seq length: 0  
Maximum DB seq length: 539

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

1: gb\_ba.\*  
2: gb\_hgt.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vl.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
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28: em\_un.\*  
29: em\_vl.\*  
30: em\_htg\_hum.\*  
31: em\_htg\_inv.\*  
32: em\_htg\_other.\*  
33: em\_htg\_mus.\*  
34: em\_htg\_pln.\*  
35: em\_htg\_rod.\*  
36: em\_htg\_nam.\*  
37: em\_htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	539	100.0	539	6	AR028492	AR028492 Sequence
2	539	100.0	539	6	BD231801	BD231801 Isolated
3	539	100.0	539	6	I55855	I55855 Sequence 18
4	539	100.0	539	6	BD132471	BD132471 Isolated,
5	527.2	97.8	532	6	AR028491	AR028491 Sequence
6	527.2	97.8	532	6	BD231800	BD231800 Isolated
7	527.2	97.8	532	6	I55854	I55854 Sequence 17
8	527.2	97.8	532	6	BD132470	BD132470 Isolated,
9	527	97.8	527	9	HSU19147	U19147 Human GAGE-
10	522.2	96.9	528	6	AX334151	AX334151 Sequence
11	522.2	96.9	528	9	HSU19145	U19145 Human GAGE-
12	519.2	96.3	524	9	HSU19146	U19146 Human GAGE-
13	515.2	95.6	524	9	AF058988	AF058988 Homo sapi
14	510.2	94.7	538	6	AR028488	AR028488 Sequence
15	510.2	94.7	538	6	BD231797	BD231797 Isolated
16	510.2	94.7	538	6	I55851	I55851 Sequence 14
17	510.2	94.7	538	6	BD132467	BD132467 Isolated,
18	504	93.5	526	6	AR275666	AR275666 Sequence
19	504	93.5	526	9	AF055474	AF055474 Homo sapi
20	502.8	93.3	528	6	AR275665	AR275665 Sequence
21	502.8	93.3	528	9	AF055473	AF055473 Homo sapi
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23	356.2	66.1	430	6	AX886264	AX886264 Sequence
24	356.2	66.1	430	6	BD025874	BD025874 Sequence
25	303	56.2	530	6	AX284300	AX284300 Sequence
26	300.8	55.8	365	6	AX284692	AX284692 Sequence
27	175.8	32.6	493	9	HSA318881	AX318881 Homo sapi
28	173.2	32.1	494	6	AX921771	AX921771 Sequence
29	156	28.9	506	6	AR415772	AR415772 Sequence
30	156	28.9	506	6	BD111325	BD111325 EST and e
31	152.2	28.2	441	12	BT007722	BT007722 Synthetic
32	139.2	25.8	494	6	AR416094	AR416094 Sequence
33	139.2	25.8	494	6	BD111647	BD111647 EST and e
34	136.6	25.3	500	9	BC054022	BC054022 Homo sapi
35	134.8	25.0	475	6	AX226497	AX226497 Sequence
36	131.2	24.3	524	6	AR416095	AR416095 Sequence
37	131.2	24.3	524	6	BD111648	BD111648 EST and e
38	121.2	22.5	448	6	AX226538	AX226538 Sequence
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40	113	21.0	529	9	BC009538	BC009538 Homo sapi
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43	109.6	20.3	399	6	AR406213	AR406213 Sequence
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ALIGNMENTS

RESULT 1  
AR028492

LOCUS AR028492 539 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 18 from patent US 5858689.

ACCESSION AR028492

VERSION AR028492.1 GI:5940465

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 539)  
van der Bruggen,P., van den Eynde,B., DeBacker,O. and  
Boon-Falleur,T.  
Isolated peptides derived from the gage tumor rejection antigen  
precursor and uses thereof

TITLE

JOURNAL Patent: US 585689-A 18 12-JAN-1999;  
FEATURES Location/Qualifiers  
source 1..539  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 539; DB 6; Length 539;  
Best Local Similarity 100.0%; Pred. No. 3.2e-128;  
Matches 539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGGAGCTGTGAGCAGTGTGTGTTCTCTCCGTCGGACTCTTTTCCCTCTAC 60  
DB 1 GCCAGGAGCTGTGAGCAGTGTGTGTTCTCTCCGTCGGACTCTTTTCCCTCTAC 60  
QY 61 TGAGATTCACTCTGTGAATATAGTTGGCGAGGAGATCGACCTATTATTTGGCCTAGA 120  
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DB 121 CCAAGGCGCTATGTACAGCCTCTCTGAAGTGTATGGGCTATGGCGCCGAGCAGTTCAGT 180  
QY 181 GATGAAGTGAACACAGCAACACCTGAAGAGGGGAAACAGCACTCAACGTCAGGATCCT 240  
DB 181 GATGAAGTGAACACAGCAACACCTGAAGAGGGGAAACAGCACTCAACGTCAGGATCCT 240  
QY 241 GCAGCTCTCAGGAGGAGAGGATGAGGAGCATCTCAGGTCAAGGCGCGAGCCTGAA 300  
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QY 361 GGGCAGGAGTGTGAAGAGACACGTTGAAATGATGAGGCTGTCTCTATGTTGGAAT 480  
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QY 421 CAATCAGAGTGTGAAGAGACACGTTGAAATGATGAGGCTGTCTCTATGTTGGAAT 480  
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QY 481 TTGTTCAATAAATTTCTCCCAATAAGCTTTACAGCTTCTGCAAAAAA 539  
DB 481 TTGTTCAATAAATTTCTCCCAATAAGCTTTACAGCTTCTGCAAAAAA 539

RESULT 3  
LOCUS 155855  
DEFINITION Sequence 18 from patent US 5648226.  
ACCESSION 155855  
VERSION 155855.1 GI:2476649  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 539)  
AUTHORS Van den Eynde,B., DeBacker,O. and Boon-Falleur,T.  
TITLE Isolated peptides derived from tumor rejection antigens, and their use  
JOURNAL Patent: US 5648226-A 18 15-JUL-1997;  
FEATURES Location/Qualifiers  
source 1..539  
/organism="unknown"

JOURNAL Patent: US 585689-A 18 12-JAN-1999;  
FEATURES Location/Qualifiers  
source 1..539  
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ORIGIN

Query Match 100.0%; Score 539; DB 6; Length 539;  
Best Local Similarity 100.0%; Pred. No. 3.2e-128;  
Matches 539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGGAGCTGTGAGCAGTGTGTGTTCTCTCCGTCGGACTCTTTTCCCTCTAC 60  
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DB 61 TGAGATTCACTCTGTGAATATAGTTGGCGAGGAGATCGACCTATTATTTGGCCTAGA 120  
QY 121 CCAAGGCGCTATGTACAGCCTCTCTGAAGTGTATGGGCTATGGCGCCGAGCAGTTCAGT 180  
DB 121 CCAAGGCGCTATGTACAGCCTCTCTGAAGTGTATGGGCTATGGCGCCGAGCAGTTCAGT 180  
QY 181 GATGAAGTGAACACAGCAACACCTGAAGAGGGGAAACAGCACTCAACGTCAGGATCCT 240  
DB 181 GATGAAGTGAACACAGCAACACCTGAAGAGGGGAAACAGCACTCAACGTCAGGATCCT 240  
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DB 301 GCTGATAGCCAGAACAGGGTCAACAGAGTGTGAAGTGTGAAGTGTCTCTGAT 360  
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DB 481 TTGTTCAATAAATTTCTCCCAATAAGCTTTACAGCTTCTGCAAAAAA 539

RESULT 2  
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LOCUS Isolated polypeptides binding with HLA-A29 molecule, nucleic acids  
DEFINITION as molecules encoding the same, and utilization thereof.  
ACCESSION BD231801  
VERSION BD231801.1 GI:33041571  
KEYWORDS JP 2002509859-A/11.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 539)  
AUTHORS Bruggen,P.V.D., Eynde,B.V.D., Debacker,O. and Falleur,T.B.  
TITLE Isolated polypeptides binding with HLA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof  
JOURNAL Patent: JP 2002509859-A 11 02-APR-2002;  
COMMENT LUDWIG INSTITUTE FOR CANCER RESEARCH  
OS Homo sapiens (human)  
PN JP 2002509859-A/11  
PD 02-APR-2002  
PF 12-JAN-1999 JP 2000528586  
PR 23-JAN-1998 US 09/012818  
PI PIERRE VAN DER BRUGEN,BENOIT VAN DEN EYNDE,OLIVIER DEBACKER,  
PI THIERRY BOON FALLEUR



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/db_xref="taxon:32630"

ORIGIN
Query Match 100.0%; Score 539; DB 6; Length 539;
Best Local Similarity 100.0%; Pred. No. 3.2e-128;
Matches 539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGGAGCTGTGAGGAGTGTCTGTGGTTCCTGCCGTCGGACTCTTTTCTCTAC 60
DB 1 GCCAGGAGCTGTGAGGAGTGTCTGTGGTTCCTGCCGTCGGACTCTTTTCTCTAC 60
QY 61 TGAGATTCACTGTGGAATATGAGTTCGGCAGAGATGACCTATTATTGGCCTAGA 120
DB 61 TGAGATTCACTGTGGAATATGAGTTCGGCAGAGATGACCTATTATTGGCCTAGA 120
QY 121 CCAAGGCGCTATGTACAGCTCTCTGAAGTGATTGGGCTTATGCGGCCGAGCAGTTCAGT 180
DB 121 CCAAGGCGCTATGTACAGCTCTCTGAAGTGATTGGGCTTATGCGGCCGAGCAGTTCAGT 180
QY 181 GATGAAGTGAACACAGCAACCTGAAGAGGGAAACAGCAACTCAACGTCAGGATCCT 240
DB 181 GATGAAGTGAACACAGCAACCTGAAGAGGGAAACAGCAACTCAACGTCAGGATCCT 240
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QY 481 TTGTTCAATTAATTTCTCCCAATAAGCTTTACAGCTTCTGCAAAAAA 539
DB 481 TTGTTCAATTAATTTCTCCCAATAAGCTTTACAGCTTCTGCAAAAAA 539

RESULT 5
AR028491 LOCUS
DEFINITION Sequence 17 from patent US 5858689.
ACCESSION AR028491
VERSION AR028491.1 GI:5940464
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 532)
van der Bruggen, P., van den Eynde, B., DeBacker, O. and Boon-Falleur, T.
TITLE Isolated peptides derived from the gage tumor rejection antigen precursor and uses thereof
JOURNAL Patent: US 5858689-A 17 12-JAN-1999;
FEATURES Location/Qualifiers
source 1..532
/mol_type="unknown"
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ORIGIN
Query Match 97.8%; Score 527.2; DB 6; Length 532;
Best Local Similarity 99.4%; Pred. No. 3.6e-125;
Matches 529; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 ACCTGTAGGAGTGTGTGTGGTTCCTGCCGTCGGACTCTTTTCTCTAGATT 67

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ORIGIN
Query Match 100.0%; Score 539; DB 6; Length 539;
Best Local Similarity 100.0%; Pred. No. 3.2e-128;
Matches 539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGGAGCTGTGAGGAGTGTCTGTGGTTCCTGCCGTCGGACTCTTTTCTCTAC 60
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QY 61 TGAGATTCACTGTGGAATATGAGTTCGGCAGAGATGACCTATTATTGGCCTAGA 120
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QY 421 CAATCAGTGTAAAGAGACAGTGAATGATGAGGTCGCTCTATGTTGAAAT 480
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DB 481 TTGTTCAATTAATTTCTCCCAATAAGCTTTACAGCTTCTGCAAAAAA 539

RESULT 4
BD132471 LOCUS
DEFINITION Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof.
ACCESSION BD132471
VERSION BD132471.1 GI:23227416
KEYWORDS JP 2002507112-A/11.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE artificial sequences.
AUTHORS 1 (bases 1 to 539)
DeBacker, O., Eynde, B.V.D. and Falleur, T.B.
TITLE Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof
JOURNAL Patent: JP 2002507112-A 11 05-MAR-2002;
COMMENT LUDWIG INSTITUTE FOR CANCER RESEARCH
PN JP 2002507112-A/11
PD 05-MAR-2002
PF 23-JUN-1997 JP 1998503430
PR 24-JUN-1996 US 08/669161
PI OLIVIER DEBACKER, BENOIT VAN DEN EYNDE, THIERRY BOON FALLEUR PC
A61K38/00,A61K45/05,C07K14/82,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
source 1..539
/mol_type="synthetic construct"

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Qy 128 GCTATGTACAGCTCTCTGAAGTGTATGGGCTATGCGGCCCGAGCAGTTCAGTGATGAAG 187
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Db 181 TGGAAACAGCAACACCTGAAAGAGGAAACAGCAACTCAACGTCAGAGATCTTGCAGCTG 240
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Db 241 CTGAGGAGGAGGAGTGGGAGCATCTGCGGTGTGAGTGTGAAGATGGTCTGATGGGAGG 300
Qy 308 GCCAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGGAGG 367
Db 301 GCCAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGGAGG 360
Qy 368 AGGTGGACCCGCCAAATCCAGAGAGGTGAAACGCCCTGAAAGAGGTGAAAGCAATCAC 427
Db 361 AGATGGACCCGCCAAATCCAGAGAGGTGAAACGCCCTGAAAGAGGTGAAAGCAATCAC 420
Qy 428 AGTGTAAAAGAGACACAGTGAATGATGAGGCTGCTCTATGTTGGAATTTGTTCA 487
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Db 481 TTAATAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAAAAGGCAAAAAA 532

RESULT 6
BD231800 532 bp DNA linear PAT 17-JUL-2003
LOCUS Isolated polypeptides binding with HLA-A29 molecule, nucleic acids
DEFINITION as molecules encoding the same, and utilization thereof.
VERSION BD231800.1 GI:33041570
KEYWORDS JP 2002509859-A/10.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 532)
Bruggen,P.V.D., Eynde,B.V.D., DeBacker,O. and Falleur,T.B.
Isolated polypeptides binding with HLA-A29 molecule, nucleic acids
as molecules encoding the same, and utilization thereof
Patent: JP 2002509859-A 10 02-APR-2002;
LUDWIG INSTITUTE FOR CANCER RESEARCH
OS Homo sapiens (human)
PN JP 2002509859-A/10
PD 02-APR-2002
PF 12-JAN-1999 JP 2000528586
PR 23-JAN-1998 US 09/012818
PI PIERRE VAN DER BRUGGEN,BENOIT VAN DEN EYNDE,OLIVIER DEBACKER,
PI THIERRY BOON FALLSUR
PC C07K4/12,C12N15/09,C12P21/00,C12Q1/02,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
CC STRANDEDNESS:single,TOPOLOGY:linear
FH Key Location/Qualifiers
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FT Location/Qualifiers
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ORIGIN
Query Match 97.8%; Score 527.2; DB 6; Length 532;
Best Local Similarity 99.4%; Pred. No. 3.6e-125;
Matches 529; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 8 AGCTGTGAGGAGCTGTGTGGTTCTGCGCTCCGGACTCTTTTCTCTACTGAGATT 67
Db 1 AGCTGTGAGGAGCTGTGTGGTTCTGCGCTCCGGACTCTTTTCTCTACTGAGATT 60
Qy 68 CATCTGTGTAATATGAGTTGGCGAGAGATGACCTATTATTGGCCCTAGACCAAGC 127
Db 61 CATCTGTGTGAAATATGAGTTGGCGAGAGATGACCTATTATTGGCCCTAGACCAAGC 120
Qy 128 GCTATGTACAGCTCTCTGAAGTGTATGGGCTATGCGGCCCGAGCAGTTCAGTGATGAAG 187
Db 121 GCTATGTACAGCTCTCTGAAGTGTATGGGCTATGCGGCCCGAGCAGTTCAGTGATGAAG 180
Qy 188 TGGAAACAGCAACACCTGAAAGAGGAAACAGCAACTCAACGTCAGAGATCTTGCAGCTG 247
Db 181 TGGAAACAGCAACACCTGAAAGAGGAAACAGCAACTCAACGTCAGAGATCTTGCAGCTG 240
Qy 248 CTGAGGAGGAGGAGTGGGAGCATCTGCGGTGTGAGTGTGAAGATGGTCTGATGGGAGG 307
Db 241 CTGAGGAGGAGGAGTGGGAGCATCTGCGGTGTGAGTGTGAAGATGGTCTGATGGGAGG 300
Qy 308 GCCAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGGAGG 367
Db 301 GCCAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGGAGG 360
Qy 368 AGGTGGACCCGCCAAATCCAGAGAGGTGAAACGCCCTGAAAGAGGTGAAAGCAATCAC 427
Db 361 AGATGGACCCGCCAAATCCAGAGAGGTGAAACGCCCTGAAAGAGGTGAAAGCAATCAC 420
Qy 428 AGTGTAAAAGAGACACAGTGAATGATGAGGCTGCTCTATGTTGGAATTTGTTCA 487
Db 421 AGTGTAAAAGAGGACAGTGAATGATGAGGCTGCTCTATGTTGGAATTTGTTCA 480
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Db 481 TTAATAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAAAAGGCAAAAAA 532

RESULT 7
LOCUS I55854 532 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 17 from patent US 5648226.
ACCESSION I55854
VERSION I55854.1 GI:2476648
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 532)
AUTHORS Van den Eynde,B., DeBacker,O. and Boon-Falleur,T.
TITLE Isolated peptides derived from tumor rejection antigens, and their use
JOURNAL Patent: US 5648226-A 17 15-JUL-1997;
FEATURES
source 1..532 /organism='unknown'
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ORIGIN
Query Match 97.8%; Score 527.2; DB 6; Length 532;
Best Local Similarity 99.4%; Pred. No. 3.6e-125;
Matches 529; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 8 AGCTGTGAGGAGCTGTGTGGTTCTGCGCTCCGGACTCTTTTCTCTACTGAGATT 67
Db 1 AGCTGTGAGGAGCTGTGTGGTTCTGCGCTCCGGACTCTTTTCTCTACTGAGATT 60
Qy 68 CATCTGTGTAATATGAGTTGGCGAGAGATGACCTATTATTGGCCCTAGACCAAGC 127
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Db      121 GCTATGTACAGCTCTCTGAAAGTATGGGCTATGCGGCCGAGCAGTTCTAGTGTAGAG 180
QY      188 TGGACACGACACCTCTGAAGAGGGGAACAGCAACTCAACGTCAGGATCCTGCAGCTG 247
Db      181 TGGAACACGACACCTCTGAAGAGGGGAACAGCAACTCAACGTCAGGATCCTGCAGCTG 240
QY      248 CTCAGGAGGAGAGGATGAGGAGGATCTGCAGGTCGAAGGCCGAGCCTGAAGCTGATA 307
Db      241 CTCAGGAGGAGAGGATGAGGAGGATCTGCAGGTCGAAGGCCGAGCCTGAAGCTGATA 300
QY      308 GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGTGAGGCGAGG 367
Db      301 GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGTGAGGCGAGG 360
QY      368 AGGTGGACCCGCAATCCAGAGGAGGTGAACACCCCTGAAGAGGTGAAGAGCAATCAC 427
Db      361 AGATGGACCCGCAATCCAGAGGAGGTGAACACCCCTGAAGAGGTGAAGAGCAATCAC 420
QY      428 AGTGTAAAGAGACACGCTTGAAATGATGCGAGGCTGCTCTATGTTGAAATTTGTTCA 487
Db      421 AGTGTAAAGAGACACGCTTGAAATGATGCGAGGCTGCTCTATGTTGAAATTTGTTCA 480
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## RESULT 8

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BD132470
LOCUS      BD132470          532 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Isolated, nucleic acid molecules which code for GAGE tumor
rejection antigen, the tumor rejection antigen, and uses thereof.
ACCESSION BD132470
VERSION   BD132470.1 GI:23227415
KEYWORDS  JP 2002507112-A/10.
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE 1 (bases 1 to 532)
AUTHORS   Debacker, O., Bynde, B.V.D. and Falleur, T.B.
TITLE      Isolated, nucleic acid molecules which code for GAGE tumor
rejection antigen, the tumor rejection antigen, and uses thereof
JOURNAL    Patent: JP 2002507112-A 10 05-MAR-2002;
LUDWIG INSTITUTE FOR CANCER RESEARCH
COMMENT    PN JP 2002507112-A/10
PD         05-MAR-2002
PF         23-JUN-1997 JP 1998503430
PI         24-JUN-1996 US 08/669161
PI         OLIVIER DEBACKER, BENOIT VAN DEN EYNDE, THIERRY BOON FALLEUR PC
AG1K38/00, AG1K45/05, C07K14/82, C12N15/00 CC
Strandedness: Single;
CC         Topology: Linear;
FH         Key Location/Qualifiers.
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## ORIGIN

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Query Match      97.8%; Score 527.2; DB 6; Length 532;
Best Local Similarity 99.4%; Pred. No. 3.6e-125;
Matches 529; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      8 AGCTGTGAGCAGTGTGTGTTCTCTGCGGTCGAGACTCTTTTCTCTACTGAGATT 67
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Db      61 CATCTGTGTAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGC 120
QY      128 GCTATGTACAGCTCTCTGAAAGTATGGGCTATGCGGCCGAGCAGTTCTAGTGTAGAG 187
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QY      248 CTCAGGAGGAGAGGATGAGGAGGATCTGCAGGTCGAAGGCCGAGCCTGAAGCTGATA 307
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QY      368 AGGTGGACCCGCAATCCAGAGGAGGTGAACACCCCTGAAGAGGTGAAGAGCAATCAC 427
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QY      428 AGTGTAAAGAGACACGCTTGAAATGATGCGAGGCTGCTCTATGTTGAAATTTGTTCA 487
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Db      481 TTAATAATCTCCATAAAGCTTTACAGCTTCTGCAAAAAA 532

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## RESULT 9

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HSU19147
LOCUS      Human GAGE-6 protein mRNA, complete cds.
DEFINITION
ACCESSION U19147
VERSION   U19147.1 GI:914908
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 527)
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE      A new family of genes coding for an antigen recognized by
autologous cytolytic T lymphocytes on a human melanoma
JOURNAL    J. Exp. Med. 182 (3), 689-698 (1995)
MEDLINE   95378788
PUBMED    7544395
REFERENCE 2 (bases 1 to 527)
AUTHORS   Van Den Eynde, B.J.
TITLE      Direct Submission
JOURNAL    Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute
for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium
FEATURES   Location/Qualifiers
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ORIGIN
Query Match      96.9%; Score 522.2; DB 9; Length 528;
Best Local Similarity 99.4%; Pred. No. 6.9e-124;
Matches 524; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAGGGAGCTGTGAGGAGTGTGTGTCTCTCCGCTCCGACTCTTTTCTCTCTAC 60
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Db 242 GCAGCTGTCTCAGAGGAGAGGATGAGGAGCATCTGCAGGTCAGGGCCGAGCCTGAA 301
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Db 302 GCTGATAGCCAGGAAACAGGCTCACCCACAGACTGGGTGTGAGTGTAAGATGGTCTCTGAT 361
QY 361 GGGCAGGAGTGGACCCGCAATCCAGAGGAGGTGAAACGCTGAAAGAGTGAAGAAG 420
Db 362 GGGCAGGAGTGGACCCGCAATCCAGAGGAGGTGAAACGCTGAAAGAGTGAAGAAG 421
QY 421 CAATCACAGTGTAAAGAGACAGCTTGAAATGATGAGGCTGTCTCTATGTTGGAAT 480
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QY 481 TTGTTTCATTAAATTTCTCCCAATAAGCTTTTACAGCTTTCTGCAAAA 527
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RESULT 12
HSU19146      524 bp mRNA linear PRI 04-DEC-1995
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Van den Eynde,B., Peeters,O., De Backer,O., Gaugler,B., Lucas,S.
and Boon,T.
A new family of genes coding for an antigen recognized by
autologous cytolytic T lymphocytes on a human melanoma
J. Exp. Med. 182 (3), 689-698 (1995)
95378788
PUBMED
7544395
REFERENCE
2 (bases 1 to 524)
AUTHORS
Van Den Eynde,B.J.
TITLE
Direct Submission
JOURNAL
Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute
for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium
LOCATION/Qualifiers
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CDS
Query Match      96.3%; Score 519.2; DB 9; Length 524;
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Matches 521; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 AGCTGTGAGGCACTGCTGTGTGTTCTCTCCGCTCCGACTCTTTTCTCTCTACTGAGATT 67
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QY 128 GCTATGTACAGCTCTCTGAAGTGATTGGCCCTATCGGCCCGAGCAGTTCAGTGTGAAG 187
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QY 248 CTCAGAGGGAGAGATGAGGAGCATCTGCAGGTCAGGGCCGAGCCTGAAAGCTGATA 307
Db 241 CTCAGAGGGAGAGATGAGGAGCATCTGCAGGTCAGGGCCGAGCCTGAAAGCTGATA 300
QY 308 GCCAGGAACAGGCTCACCCACAGCTGGGTGTGAGTGTGAAGATGCTCTGATGGSCAGG 367
Db 301 GCCAGGAACAGGCTCACCCACAGCTGGGTGTGAGTGTGAAGATGCTCTGATGGSCAGG 360
QY 368 AGTGGACCCGCCAAATCCAGAGGAGGTGAAACCGCTGAAAGAGGTGAAAAAGCAATCAC 427
Db 361 AGATGGACCCGCCAAATCCAGAGGAGGTGAAACCGCTGAAAGAGGTGAAAAAGCAATCAC 420
QY 428 AGTGTAAAGNAGACAGCTTGAATATGATGAGGCTGTCTCTATGTTGAAATTTGTTCA 487
Db 421 AGTGTAAAGNAGACAGCTTGAATATGATGAGGCTGTCTCTATGTTGAAATTTGTTCA 480
QY 488 TTAATAATTTCTCCCAATAAGCTTTTACAGCTTTCTCAAAAAAAA 531
Db 481 TTAATAATTTCTCCCAATAAGCTTTTACAGCTTTCTCAAAAAAAA 524

RESULT 13
AF058988
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Chen,M.E., Lin,S.-H., Chung,L.W.K. and Sikes,R.A.
Isolation and characterization of PAGE-1 and GAGE-7: new genes
expressed in the LNCaP prostate cancer progression model that share
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JOURNAL homology with melanoma associated antigens  
REFERENCE J. Biol. Chem. (1998) In press  
2. (bases 1 to 524)  
AUTHORS Chen,M.E., Lin,S.-H., Chung,L.W.K. and Sikes,R.A.  
TITLE Direct Submission  
JOURNAL Submitted (07-APR-1998) Urology, University of Virginia, Box 422,  
Charlottesville, VA 22908, USA  
FEATURES Location/Qualifiers  
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insensitive in the human prostate cancer progression model  
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ORIGIN

Query Match 95.6%; Score 515.2; DB 9; Length 524;  
Best Local Similarity 98.7%; Pred. No. 4.4e-122;  
Matches 517; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
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Qy 63 AGATTCTCTGTGAATATGAGTGGCGAGGAGATGCACTATTATTGGCCCTAGACC 122  
Db 61 AGATTCTCTGTGAATATGAGTGGCGAGGAGATGCACTATTATTGGCCCTAGACC 120  
Qy 123 AAGGCGCTATACAGCCTCTGAGTGAATGGGCTTATGCGGCCGAGCAGTTCACTGA 182  
Db 121 AAGGCGCTATACAGCCTCTGAAATGATTTGGGCTTATGCGGCCGAGCAGTTCACTGA 180  
Qy 183 TGAAGTGAACACGACCTGAGAGGGGACCACTCAAGTCAAGATCTCTGATGG 242  
Db 181 TGAAGTGAACACGACCTGAGAGGGGACCACTCAAGTCAAGATCTCTGATGG 240  
Qy 243 AGCTGCTCAGGAGGAGGATGAGGAGCATCTGCAGTCAAGGGCCGAGCCTGAAGC 302  
Db 241 AGCTGCTCAGGAGGAGGATGAGGAGCATCTGCAGTCAAGGGCCGAGCCTGAAGC 300  
Qy 303 TGATAGCCAGGAACAGGGTCAACACAGACTGGGTGTGAGTGTGAAGATGCTCTGATGG 362  
Db 301 TCATAGCCAGGAACAGGGTCAACACAGACTGGGTGTGAGTGTGAAGATGCTCTGATGG 360  
Qy 363 GCAGGAGTGCACCGCCCAATCCAGAGGAGTGAACCGCTGAAGAGGTGAAGACA 422  
Db 361 GCAGGAGTGCACCGCCCAATCCAGAGGAGTGAACCGCTGAAGAGGTGAAGACA 420  
Qy 423 ATCACAGTGTAAAGAGACACAGTGTGAATGATGAGGCTGCTCTTATGTTGAAATTT 482  
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Qy 483 GTTCATTAATAATTCCTCAATAAAGCTTTACAGCTTCTGCAAA 526  
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RESULT 14

AR028488 538 bp DNA linear PAT 29-SEP-1999  
LOCUS

DEFINITION Sequence 14 from patent US 5858689.  
ACCESSION AR028488  
VERSION AR028488.1 GI:5940461  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 538)  
AUTHORS van der Bruggen,P., van den Eynde,B., DeBacker,O. and  
Boon-Falleur,I.  
TITLE Isolated peptides derived from the gage tumor rejection antigen  
precursor and uses thereof  
JOURNAL Patent: US 5858689-A 14 12-JAN-1999;  
FEATURES Location/Qualifiers  
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Query Match 94.7%; Score 510.2; DB 6; Length 538;  
Best Local Similarity 98.0%; Pred. No. 8.7e-121;  
Matches 528; Conservative 0; Mismatches 8; Indels 3; Gaps 1;  
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Qy 121 CCAAGGCGCTATGTACAGCCTCTCTGAAGTGAATGGGCTATGCGGCCGAGCAGTTCAGT 180  
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Qy 241 GCAGCTCTCAGGAGGAGGAGTGAAGGAGCATCTGCAGTCAAGGGCCGAGCCTGAA 300  
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Qy 301 GCTGATAGCCAGGAACAGGGTCAACACAGACTGGGTGTGAGTGTGAAGATGGTCTGAT 360  
Db 300 GCTCATAGCCAGGACAGGGTCAACACAGACTGGGTGTGAGTGTGAAGATGGTCTGAT 359  
Qy 361 GGGCAGGAGTGGACCCGCCAAATCCAGAGGAGTGAAGAGCGCTGAAGAGGTGAAGAG 420  
Db 360 GGGCAGGAGTGGACCCGCCAAATCCAGAGGAGTGAAGAGCGCTGAAGAGGTGAAGAG 419  
Qy 421 CAATCAGTGTAAAGAGACACAGTGTGAATGATGAGGCTGCTCTTATGTTGAAAT 480  
Db 420 CAATCAGTGTAAAGAGACACAGTGTGAATGATGAGGCTGCTCTTATGTTGAAAT 479  
Qy 481 TTGTTCAATAAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAAA 539  
Db 480 TTGTTCAATAAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAAA 538

RESULT 15

BD231797 538 bp DNA linear PAT 17-JUL-2003  
LOCUS BD231797  
DEFINITION Isolated polypeptides binding with HLA-A29 molecule, nucleic acids  
as molecules encoding the same, and utilization thereof.  
ACCESSION BD231797  
VERSION BD231797.1 GI:33041567  
KEYWORDS JP 2002509859-A/7.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 538)

AUTHORS Bruggen,P.V.D., Eynde,B.V.D., Debacker,O. and Falleur,T.B.  
TITLE Isolated polypeptides binding with HLA-A29 molecule, nucleic acids  
as molecules encoding the same, and utilization thereof  
JOURNAL Patent: JP 2002509859-A 7 02-APR-2002;  
LUDWIG INSTITUTE FOR CANCER RESEARCH  
COMMENT OS Homo sapiens (human)  
PN JP 2002509859-A/7  
PD 02-APR-2002  
PF 12-JAN-1999 JP 2000528586  
PR 23-JAN-1998 US 09/012818  
PI PIERRE VAN DER BRUGEN,BENOIT VAN DEN EYNDE,OLIVIER DERACKER,  
THIERRY BOON FALLEUR  
PC C07K4/12,C12N15/09,C12P21/00,C12Q1/02,C12N15/00 CC Isolated  
polypeptides binding with HLA-A29 molecule, nucleic CC  
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Best Local Similarity 98.0%; Pred. No. 8.7e-121;  
Matches 528; Conservative 0; Mismatches 8; Indels 3; Gaps 1;  
QY 1 GCCAGGGAGCTGTGAGGCGAGTCTGTGTGTTCTGTCGCTCCGACTCTTTTTCCTCTAC 60  
DB 3 GCCAGGGAGCTGTGAGGCGAGTCTGTGTGTTCTGTCGCTCCGACTCTTTTTCCTCTAC 62  
QY 61 TGAGATTCACTGTGTGAATATGATGTGGCGAGGAAGATCGACCTATTATTGGCCTAGA 120  
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DB 240 GCAGCTGCTCAGGAGGAGAGATGAGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAA 299  
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QY 361 GGGCAGGAGTGGACCCGCCAAATCCAGAGGAGGTGAACCGCTGAAGAGGTGAAAAG 420  
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DB 420 CAATCACAGTGTAAAGAGACAGTTGAATGATGCGGCTGCTCTATTTGGAAT 479  
QY 481 TTGTTCAATTAATTTCTCCCAATAAGCTTTACGCTTCTCAAAAAAAAAAAAAA 539  
DB 480 TTGTTCAATTAATTTCTCCCAATAAGCTTTACGCTTCTCAAAAAAAAAAAAAA 538

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Job time : 3605 secs

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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2004, 11:18:29 ; Search time 2509 Seconds

(without alignments)  
6415.191 Million cell updates/sec

Title: US-09-782-745-18

Perfect score: 539

Sequence: 1 GCCAGGAGCTGTGAGGAG.....CTGCACAAAAA 539

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapept 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 28626722

Minimum DB seq length: 0

Maximum DB seq length: 539

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: em\_esthum.\*  
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27: em\_gss\_vrl.\*  
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29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	532.2	98.7	537	12	BM832793
2	509.4	94.5	527	12	BI826605
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4	503.4	93.4	517	14	CF780547

5	492.4	91.4	509	12	BI868671
C	471.6	87.5	489	9	AA447559
C	450.6	83.6	457	10	AM510753
C	442	82.0	464	9	AA738037
C	440.6	81.7	447	9	AI381509
10	437	81.1	480	12	BG120336
11	436	80.9	505	14	CB115693
C	433.2	80.4	450	9	AA760996
C	418.6	77.7	455	9	AI187350
C	405.8	75.3	418	9	AW016546
C	397.2	73.7	426	9	AA868226
16	378.2	70.2	419	9	AA448542
17	374.6	69.5	383	12	BM836228
18	374.4	69.5	445	11	BC005363
C	362.2	67.2	412	9	AW102587
C	338	62.7	383	13	EX283580
C	331.2	61.4	384	9	AA913206
C	315.8	58.6	341	12	BP431265
C	315.6	58.6	397	12	BG206349
C	314	58.3	398	9	AA918604
C	307.8	57.1	320	12	BM836021
C	305.6	56.7	333	13	BU533718
C	274.6	50.9	457	14	CF780497
C	268.2	49.8	275	14	CB147043
C	268.2	49.8	275	14	CB150355
C	268.2	49.8	275	14	CB157288
C	245.6	45.6	256	12	BG181480
C	230.2	42.7	258	12	BG186708
C	225	41.7	253	12	BG184057
C	225	41.7	261	12	BG199060
C	221.6	41.1	245	12	BG212621
C	218.2	40.5	292	12	BG213622
C	214.8	39.9	245	12	BG208433
C	210.8	39.1	507	9	AA972716
C	207	38.4	256	12	BG216461
C	206.8	38.4	524	11	AF318372
C	204.8	38.0	224	9	AA738394
C	197.2	36.6	520	14	CB961487
C	193.8	36.0	197	9	AI968311
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C	192.4	35.7	499	12	BG354572

## ALIGNMENTS

RESULT 1	BM832793	537 bp	mRNA	linear	EST 06-MAR-2002
LOCUS	K-EST0107334	S5SNU484s1	Homo sapiens	cdna clone	S5SNU484s1-8-F10
DEFINITION	5', mRNA sequence.				
ACCESSION	BM832793	GI:19189202			
VERSION	BM832793.1	GI:19189202			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.				
TITLE	21C Frontier Korean EST Project 2001				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 8 row: F column: 10 High quality sequence stop: 537.				

FEATURES  
source

Location/Qualifiers  
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/clone="SSNU484s1-8-F10"  
/sex="M"  
/tissue\_type="Stomach"  
/cell\_type="Epithelial"  
/lab\_host="TOP10P"  
/clone\_lib="SSNU484s1"  
/note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;  
Site 2: NotI; The poly (A)+ RNA was decapped with tobacco  
acid pyrophosphatase (TAP) and ligated with DNA-RNA linker  
including EcoRI site by treatment of T4 RNA ligase. The  
first strand cDNA was synthesized from oligo dt-selected  
mRNA by priming with dt-tailed vector. The dt-tailed  
vector was adjusted to have about 60nt. The cDNA vector  
was circularized with E. coli DNA ligase after digestion  
of EcoRI which site is also included in vector. An RNA  
strand converted to a DNA strand by Okayama-Berg method.  
The obtained cDNA vectors were used for transformation of  
competent cells E. coli Top10P by electroporation method.  
After analyzing and sequencing about 2,000 ~ 3,000  
colonies in original cDNA library, the abundant cDNAs were  
selected and amplified by PCR reaction using vector region  
primer including T7 promoter as 5' primer and N(dn)14 as  
3' primer. The PCR products were used as template for  
synthesis of biotinylated single stranded RNA by in vitro  
transcription reaction. The synthesized RNA probes were  
hybridized with antisense single stranded cDNAs prepared  
from original library and incubated with avidin-gel.  
After removing DNA-RNA hybrids by centrifuge, the  
subtracted cDNA libraries were constructed by  
transformation of the remaining DNA into competent cells E.  
coli Top10P with electroporation method."

## ORIGIN

Query Match 98.7%; Score 532.2; DB 12; Length 537;  
Best Local Similarity 99.4%; Pred. No. 2.8e-98;  
Matches 534; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCAGGAGCTGTGAGGAGCTGTGTGGTCTCGCGTCCGACCTTTTCTCTAC 60  
DB 1 GCCAGGAGCTGTGAGGAGCTGTGTGGTCTCGCGTCCGACCTTTTCTCTAC 60

QY 61 TGAGATTTCATCTGTGAAATATGAGTGTGGGAGATCGACCTATTATGGCCTAGA 120  
DB 61 TGAGATTTCATCTGTGAAATATGAGTGTGGGAGATCGACCTATTATGGCCTAGA 120

QY 121 CCAAGGCGCTATGTACAGCCTCTGAAAGTGATTGGGCTATGCGGCCGAGCAGTTCAGT 180  
DB 121 CCAAGGCGCTATGTACAGCCTCTGAAAGTGATTGGGCTATGCGGCCGAGCAGTTCAGT 180

QY 181 GATGAAGTGAACACAGCAACACCTGAAAGAGGGAACACGACCTCAACGTCAGGATCCT 240  
DB 181 GATGAAGTGAACACAGCAACACCTGAAAGAGGGAACACGACCTCAACGTCAGGATCCT 240

QY 241 GCAGCTCTCAGAGGAGGAGGATGAGGAGCATCTCAGGTCAAGGCCGAGCCTGAA 300  
DB 241 GCAGCTCTCAGAGGAGGAGGATGAGGAGCATCTCAGGTCAAGGCCGAGCCTGAA 300

QY 301 GCTGATAGCCAGGAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGAT 360  
DB 301 GCTCATAGCCAGGAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGAT 360

QY 361 GGGCAGAGAGTGACCCGCCAATTCAGAGAGAGTGAAACCGCTGAAGAGGTGAAAG 420  
DB 361 GGGCAGAGAGTGACCCGCCAATTCAGAGAGAGTGAAACCGCTGAAGAGGTGAAAG 420

QY 421 CAATCAGTGTAAAGAGACACGTTGAAATGATGACGCTGCTCTATGTTGGAAT 480  
DB 421 CAATCAGTGTAAAGAGACACGTTGAAATGATGACGCTGCTCTATGTTGGAAT 480

## Db

421 CAATCAGTGTAAAGAGACACGTTGAAATGATGACGCTGCTCTATGTTGGAAT 480  
QY 481 TTGTTCTATAAAATCTCCCAATAAAGCTTTACAGCCTCTCGCAAAAAA 537  
DB 481 TTGTTCTATAAAATCTCCCAATAAAGCTTTACAGCCTCTCGCAAAAAA 537

## RESULT 2

BI826605 527 bp mRNA linear EST 04-OCT-2001  
LOCUS 603077056F1 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:516892 5',  
DEFINITION mRNA sequence.  
ACCESSION BI826605  
VERSION BI826605.1 GI:15938155  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 527)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM11419 row: p column: 13  
High quality sequence stop: 519.

FEATURES  
source

Location/Qualifiers  
1. .527  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:516892"  
/tissue\_type="medulla"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_119"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: EcoRV (destroyed); RNA source normal medulla from  
anonymous male age 27. Library is oligo-dT primed and  
directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.3 kb, insert size range  
0.9-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 013. Note:  
this is a NIH\_MGC Library."

## ORIGIN

Query Match 94.5%; Score 509.4; DB 12; Length 527;  
Best Local Similarity 97.9%; Pred. No. 1.2e-93;  
Matches 516; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 10 CTGTGAGGAGTCTGTGTGGTCTCGCGCTCGGACTCTTTTCTCTACTGAGATCA 69  
DB 1 CTGTGAGGAGTCTGTGTGGTCTCGCGCTCGGACTCTTTTCTCTACTGAGATCA 60

QY 70 TCTGTGTAATATGAGTGTGGGAGGAAGATGACCTATTATTGGCTAGCAAGCGC 129  
DB 61 TCTGTGTAATATGAGTGTGGGAGGAAGATGACCTATTATTGGCTAGCAAGCGC 120

QY 130 TATGTACAGCCTCTGAAAGTATTGGCCCTATGCGGCCGAGCAGTTCAGTGAAGTG 189  
DB 121 TATGTACAGCCTCTGAAAGTATTGGCCCTATGCGGCCGAGCAGTTCAGTGAAGTG 180

QY 190 GAACAGGACACCTCAAGAGGGGAACCAAGCACTCAAGCTCAGGATCTCGAGCTGCT 249  
DB 181 GAACAGGACACCTCAAGAGGGGAACCAAGCACTCAAGCTCAGGATCTCGAGCTGCT 240

```

QY 250 CAGGAGGAGGATGAGGAGGATCTGCAGCTCAAGGCGGAGCCTGAAGCTGTAGC 309
    |||
Db 241 CAGAGGGAGAGATGAGGAGGATCTGCAGGTCAGGGCGGAGCCTGAAGCTCATAGC 300
    |||
QY 310 CAGGAACAGGGTCACCCACACAGACTGGGTGTGAGTGTGAAGATGGTCTCGATGGCGAGGAG 369
    |||
Db 301 CAGGAACAGGGTCACCCACACAGACTGGGTGTGAGTGTGAAGATGGTCTCGATGGCGAGGAG 360
    |||
QY 370 GTGACCCCGCAATCCAGAGGAGGTGAAACGCTGGAAGAGGTGAAAGCAATCACAG 429
    |||
Db 361 ATGGACCCCGCAATCCAGAGGAGGTGAAACGCTGGAAGAGGTGAAAGCAATCACAG 420
    |||
QY 430 TGTATAAAGAACACAGCTTGAATGATGCAGGCTGCTCTATCTGTGAAATTTGTTCAAT 489
    |||
Db 421 TGTATAAAGAGGACAGCTTGAATGATGCAGGCTGCTCTATCTGTGAAATTTGTTCAAT 480
    |||
QY 490 AAAATTCCTCCAAATAAGCTTTACAGCTTCTGCAAAAAA 536
    |||
Db 481 AAAATTCCTCCAAATAAGCTTTACAGCTTCTGCAAAAAA 527
    |||

```

## RESULT 3

```

BX108227
LOCUS
DEFINITION
  BX108227 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE998K213161 ;
  IMAGE:1256204, mRNA sequence.

```

```

ACCESSION
  BX108227
VERSION
  BX108227.1
KEYWORDS
  EST.
SOURCE
  GI:27835080

```

```

ORGANISM
  Homo sapiens (human)

```

```

REFERENCE
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

AUTHORS
  Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
  Radelof,J., Schneider,D. and Korn,B.

```

```

TITLE
  Human Unigeneset - RZPD3

```

```

JOURNAL
  Unpublished (2003)

```

```

COMMENT
  Contact: Ina Rolfs

```

```

  RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

```

```

  Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

```

```

  RZPD; IMAGE998K213161.

```

```

  RZPDLIB; I.M.A.G.E. cDNA Clone Collection;

```

```

  Human Unigeneset - RZPD3 (RZPDLIB No.972)

```

```

  http://www.rzpd.de/CloneCards/cgi-

```

```

  bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs

```

```

  RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

```

```

  Heubnerweg 6, D-14059 Berlin, Germany

```

```

  Tel: +49 30 32639 101

```

```

  Fax: +49 30 32639 111

```

```

  www.rzpd.de

```

```

  This clone is available royalty-free from RZPD;

```

```

  contact RZPD (clone@rzpd.de) for further information. Seq primer:

```

```

  M13r, Primer sequence: TTTCACAGGAACAGCTATGAC.

```

## FEATURES

```

  source

```

```

    1..521
      /organism="Homo sapiens"

```

```

      /mol_type="mRNA"

```

```

      /db_xref="taxon:9606"

```

```

      /clone="IMAGE998K213161 ; IMAGE:1256204"

```

```

      /tissue_type="pooled germ cell tumors"

```

```

      /lab_host="DH10B"

```

```

      /clone_lib="NCI_CGAP GC3"

```

```

      /note="Vector: pTZ19-Lac (Pharmacia) with a modified

```

```

      polylinker; 1st strand cDNA was prepared from 3 pooled

```

```

      germ cell tumors, and was then primed with a Not I -

```

```

      oligo(dT) primer. Double-stranded cDNA was ligated to Eco

```

```

      RI adaptors (Pharmacia), digested with Not I and cloned

```

```

      into the Not I and Eco RI sites of the modified pTZ19

```

```

      vector. Library is not normalized. Library was

```

```

      constructed by Bento Soares and M. Fatima Bonaldo. "

```

## ORIGIN

```

Query Match      94.4%; Score 508.8; DB 13; Length 521;
Best Local Similarity 98.7%; Pred. No. 1.6e-93;
Matches 513; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 18 CAGTGTGTGTGTTCTCTGCGGTCGCGACTCTTTTCTCTACTGAGATTCATCTGTGTG 77
    |||
Db 1 CAGTGTGTGTGTTCTCTGCGGTCGCGACTCTTTTCTCTACTGAGATTCATCTGTGTG 60
    |||
QY 78 AAATATGAGTGTGCGAGGAAGATCGACCTATTATTGCGCTTAGACCAAGGCGCTATGTACA 137
    |||
Db 61 AAATATGAGTGTGCGAGGAAGATCGACCTATTATTGCGCTTAGTCCAGACGCTATGTACA 120
    |||
QY 138 GCCTCTCTGAAGTCATTGGGCGCTATGCGGCCGAGAGGATTCAGTGATGAAGTGAACACAG 197
    |||
Db 121 GCCTCTCTGAATGATTGGGCGCTATGCGGCCGAGAGGATTCAGTGATGAAGTGAACACAG 180
    |||
QY 198 AACACCTCTGAAGAGGGGAACCGACCACTCAACCTCAGGATCCTGCGAGCTGCTCAGGAGGG 257
    |||
Db 181 AACACCTCTGAAGAGGGGAACCGACCACTCAACCTCAGGATCCTGCGAGCTGCTCAGGAGGG 240
    |||
QY 258 AGAGGATGAGGAGCATCTGCGAGTCAAGGCGCGAAGCCTGAGCTGTATAGCCAGGAACA 317
    |||
Db 241 AGAGGATGAGGAGCATCTGCGAGTCAAGGCGCGAAGCCTGAGCTGTATAGCCAGGAACA 300
    |||
QY 318 GGGTCACCCACACAGACTGGGTGTGAGTGTGAAGTGTCTCTGATGGGAGGAGGTGAGACC 377
    |||
Db 301 GGGTCACCCACACAGACTGGGTGTGAGTGTGAAGTGTCTCTGATGGGAGGAGGTGAGACC 360
    |||
QY 378 GCCAAATCAGAGGAGGTGAAAACGCTGAAAGAGTGAAGCAATCACAGTGTAAAA 437
    |||
Db 361 GCCAAATCAGAGGAGGTGAAAACGCTGAAAGAGTGAAGCAATCACAGTGTAAAA 420
    |||
QY 438 GAAGCACACTTGAAATGATGCGAGGCTGCTCTATGTTGAAATTTGTTCAATAATTTCT 497
    |||
Db 421 GAAGCACACTTGAAATGATGCGAGGCTGCTCTATGTTGAAATTTGTTCAATAATTTCT 480
    |||
QY 498 CCCAATAAGCTTTACAGCCTTCTGCAAAAAA 537
    |||
Db 481 CCCAATAAGCTTTTACAGCCTTCTGCAAAAAA 520
    |||

```

## RESULT 4

```

CF780547
LOCUS
DEFINITION
  IMAGE:30524555 5', mRNA sequence.

```

```

ACCESSION
  CF780547
VERSION
  CF780547.1
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)

```

```

ORGANISM
  Homo sapiens

```

```

  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

  1..(bases 1 to 517)

```

```

  NIH-MGC http://mgi.nci.nih.gov/.

```

```

  National Institutes of Health, Mammalian Gene Collection (MGC)

```

```

  Unpublished (1999)

```

```

  Contact: Daniela S. Gerhard, Ph.D.

```

```

  Office of Cancer Genomics

```

```

  National Cancer Institute / NIH

```

```

  Bldg. 31 Rm10A07 Bethesda, MD 20892

```

```

  Email: cgapbs-r@mail.nih.gov

```

```

  Tissue Procurement: James Martin, University of Iowa

```

```

  cDNA Library Preparation: M. Bento Soares, University of Iowa

```

```

  DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

```

```

  DNA Sequencing by: Agencourt Bioscience Corporation

```

```

  Clone distribution: MGC clone distribution information can be

```

```

  found through the I.M.A.G.E. Consortium/LLNL at:

```

```

  http://image.llnl.gov

```

```

  Plate: NDAM604 row: e column: 12

```

```

  High quality sequence strop: 517.

```

```

  Location/Qualifiers

```

## FEATURES

```
source
1. 517
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30524555"
/tissue_type="Pooled Chondrosarcoma Tumor cells"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_217"
/notes="vector: pfx-Asc; Site 1: EcoRI; Site 2: NotI; Library is oligo-dT primed and directionally cloned. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoK I adaptor, digested with Not I and then cloned directionally into pfx-Asc vector. Average insert size 0.5-lkb. Adaptors 5' (AATTCGGCAGGAGG) 3' and 5'd (CTCTGCGCG) 3'. 3' linker sequence - GCGCGCGCTGAGAGCC T18. Sequencing primers 3' end: T3 promoter primer 5'd (ATTAACTCTCACTAAAGGA) 3'. 5' End: T7 promoter primer 5'd (TTATACATCTCACTAGGG) 3'. Average insert size 0.5-lkb. Library was constructed in the laboratory of M. Bento Soares. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 93.4%; Score 503.4; DB 14; Length 517;
Best Local Similarity 98.8%; Pred. No. 2e-92; 6; Indels 0; Gaps 0;
Matches 507; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 12 GTGAGGAGTCTGTGTGTTCTTCGCGTCCGGACTCTTTTCTCTACTGAGATTATC 71
Db 4 GAGGGGAGTCTGTGTGTTCTTCGCGTCCGGACTCTTTTCTCTACTGAGATTATC 63

Qy 72 TGTGTAAATATGATGTGGGAGGAGATCGACCTATTTTGGCTAGACCAAGCGCTA 131
Db 64 TGTGTAAATATGATGTGGGAGGAGATCGACCTATTTTGGCTAGACCAAGCGCTA 123

Qy 132 TGTACAGCTCTGAGTGATGTGGCTATCGGCCGAGCAGTTTCAGTGATGAAGTGA 191
Db 124 TGTACAGCTCTGAGTTGATGTGGCTATCGGCCGAGCAGTTTCAGTGATGAAGTGA 183

Qy 192 ACCAGCAACACTGAAGAAGGGGACCAAGCAACTCAAGTCTGAGGATCTTCAGCTGTCTCA 251
Db 184 ACCAGCAACACTGAAGAAGGGGACCAAGCAACTCAAGTCTGAGGATCTTCAGCTGTCTCA 243

Qy 252 GGAGGAGGATGAGGAGGATCTGAGGTCAGGTCAGGCGCCGAGCCTGAGCTGATAGCCA 311
Db 244 GGAGGAGGATGAGGAGGATCTGAGGTCAGGTCAGGCGCCGAGCCTGAGCTGATAGCCA 303

Qy 312 GGAACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGTCCTGATGGCAGGAGGT 371
Db 304 GGAACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGTCCTGATGGCAGGAGAT 363

Qy 372 GGACCCGCAATCCAGAGGAGGTGAAACCGCTGAAGAAGGTGAAAGCAATCACAGTG 431
Db 364 GGACCCGCAATCCAGAGGAGGTGAAACCGCTGAAGAAGGTGAAAGCAATCACAGTG 423

Qy 432 TTAAGAAGACAGCTTGAATGATGAGGTCAGGTCCTCTATGTTGAAATTTGTTCAATA 491
Db 424 TTAAGAAGACAGCTTGAATGATGAGGTCAGGTCCTCTATGTTGAAATTTGTTCAATA 483

Qy 492 AATTCCTCCATATAAGCTTTACAGCTTCTGCA 524
Db 484 AATTCCTCCATATAAGCTTTACAGCTTCTGCA 516

RESULT 5
BI868671
LOCUS 603392594Fl NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5402663 5',
DEFINITION mRNA sequence.
ACCESSION BI868671
VERSION BI868671.1 GI:16042344

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 509)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: MAM2026 row: 1 column: 24
High quality sequence stop: 509.
FEATURES
source
1. 509
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5402663"
/tissue_type="adenocarcinoma, cell_line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_90"
/notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 91.4%; Score 492.4; DB 12; Length 509;
Best Local Similarity 98.8%; Pred. No. 3.5e-90;
Matches 496; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCGAGGAGCTGTGAGGAGTGTGTGTTCTTCGCGTCCGGACTCTTTTCTCTAC 60
Db 8 GCTAGGAGCTGTGAGGAGTGTGTGTTCTTCGCGTCCGGACTCTTTTCTCTAC 67

Qy 61 TGAGATTTCATCTGTGTAATATGAGTTGGCAGGAGATCGACTATTTTGGCTAGA 120
Db 68 TGAGATTTCATCTGTGTAATATGAGTTGGCAGGAGATCGACTATTTTGGCTAGA 127

Qy 121 CCAAGGCGCTATGTACAGCTCTCGAAGTGAATGGGCTATGCGGCCGAGAGTTCAGT 180
Db 128 CCAAGGCGCTATGTACAGCTCTCGAAGTGAATGGGCTATGCGGCCGAGAGTTCAGT 187

Qy 181 GATGAAGTGGAAACAGCAACACCTGAAGAAGGGGAACAGCAACTCAAGTTCAGTCT 240
Db 188 GATGAAGTGGAAACAGCAACACCTGAAGAAGGGGAACAGCAACTCAAGTTCAGTCT 247

Qy 241 GCAGTGTCTCAGGAGGAGAGGATGAGGAGCATCTCAGGTCAAGGGCCGAAGCTGAA 300
Db 248 GCAGTGTCTCAGGAGGAGAGGATGAGGAGCATCTCAGGTCAAGGGCCGAAGCTGAA 307

Qy 301 GCTGATAGCCAGGAACAGGGTCAACCCAGACTGGGTGTGAGTGTGAAGATGGTCTGAT 360
Db 308 GCTCATAGCCAGGAACAGGGTCAACCCAGACTGGGTGTGAGTGTGAAGATGGTCTGAT 367

Qy 361 GGGCAGGAGTGGACCCGCCAAATCCAGAGAGGTGAAACGCTGAAGAAGGTGAAAG 420
Db 368 GGGCAGGAGATGGACCCGCCAAATCCAGAGAGGTGAAACGCTGAAGAAGGTGAAAG 427

Qy 421 CAATCACAGTGTAAAAAGAGACACGTTGAAATGATGAGGCTGCTCTCTATTTGGAAT 480
Db 428 CAATCACAGTGTAAAAAGAGACGTTGAAATGATGAGGCTGCTCTCTATTTGGAAT 487

Qy 481 TTGTTTCATTAATAATTTCTCCCA 502
```

```

Db      488 TTGTTCAATTAATAATTCCTCCAA 509
|||||
AA447559 489 bp mRNA linear EST 04-JUN-1997
zW8le11.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:782636
3' similar to TR:G914905 G914905 GAGE-4 PROTEIN. [1] ; mRNA
sequence.
ACCESSION AA447559.1 GI:2161229
VERSION   AA447559.1
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 489)
AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
JOURNAL   Unpublished (1997)
COMMENT   Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LML ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. Et from Amersham
High quality sequence stop: 427.
FEATURES
Location/Qualifiers
1..489
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:782636"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis NHT"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo (dT)
primer [5'
TGTATCAATCTGAAGTGGAGCGCGGCCCAATTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia) digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo."
ORIGIN
Query Match 87.5%; Score 471.6; DB 9; Length 489;
Best Local Similarity 99.0%; Pred. No. 6.1e-86;
Matches 485; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 41 CCGGACTCTTTTCTCTACTGAGATTCACTGTGTGAATATGAGTTGGCGAGGAAGAT 100
Db 489 CCGGACTCTTTTCTCTACTGAGATTCACTGTGTGAATATGAGTTGGCGAGGAAGAT 430
QY 101 CGACCTTATTGGCTAGACCAAGCGCTATGTACAGCCTCTCTGAAGTGAATGGGCCCTA 160
Db 429 CGACCTTATTGGCTAGACCAAGCGCTATGTACAGCCTCTCTGAAGTGAATGGGCCCTA 371
QY 161 TGGGGCCCGGAGAGTTCACTGATGAAGTGAACAGCAACACTGAAGAAGGGGAACAG 220
Db 370 TGGGGCCCGGAGAGTTCACTGATGAAGTGAACAGCAACACTGAAGAAGGGGAACAG 311
QY 221 CAACTCAAGTCAGGATCTCTGAGCTGCTCAGGAGGGAGGATGAGGAGCATCTCGAC 280

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```

Db      310 CAACTCAAGTCAGGATCTCTGAGCTGCTCAGAGGGAGAGGATGAGGGGATCTCGAC 251
|||||
QY 281 GTCAAGGGCCGAGCCTGAAGCTGATAGCCAGGAAACAGGGGTCAACCCACAGACTGGGTGTG 340
|||||
Db 250 GTCAAGGGCCGAGCCTGAAGCTGATAGCCAGGAAACAGGGGTCAACCCACAGACTGGGTGTG 191
|||||
QY 341 AGTGTGAAGATGTTCTCTGATGGCGCAGGAGTGGACCCGCCAAATCCAGAGGAGGTGAAA 400
|||||
Db 190 AGTGTGAAGATGTTCTCTGATGGCGCAGGAGTGGACCCGCCAAATCCAGAGGAGGTGAAA 131
|||||
QY 401 CGCCTCAAGAAGGTGAAGAAGCAATCACTGTGTAAAGAGACACCTTGAAATGATGCGAC 460
|||||
Db 130 CGCCTCAAGAAGGTGAAGAAGCAATCACTGTGTAAAGAGGACACCTTGAAATGATGCGAC 71
|||||
QY 461 GCTGCTCTCTATGTTGGAATTTGTTTCATTAATAATTCCTCAATAAAGCTTTACAGCCTTC 520
|||||
Db 70 GCTGCTCTCTATGTTGGAATTTGTTTCATTAATAATTCCTCAATAAAGCTTTACAGCCTTC 11
|||||
QY 521 TGCATAAAAAA 530
|||||
Db 10 TGCATAAAAAA 1
|||||
RESULT 7
AWS10753/c
LOCUS     AWS10753
DEFINITION hd39d05.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
IMAGE:2911881 3', similar to SM:GGB4_HUMAN Q13068 GAGE-4 PROTEIN. ;,
mRNA sequence.
ACCESSION AWS10753
VERSION   AWS10753.1 GI:7148831
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 457)
AUTHORS   NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LML ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
FEATURES
Location/Qualifiers
1..457
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2911881"
/lab_host="DH10B"
/clone_lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCT-CCAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
ORIGIN
Query Match 83.6%; Score 450.6; DB 10; Length 457;
Best Local Similarity 99.1%; Pred. No. 1.2e-81;
Matches 453; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 75 GTGAATATGAGTTGGCAGGAAGATCGACTATTATTGGCTAGACCAAGGCGCTATGT 134
Db 457 GTGAATATGAGTTGGCAGGAAGATCGACTATTATTGGCTAGACCAAGGCGCTATGT 398
QY 135 ACAGCTTCCTGAAGTATTTGGGCTTATGCGGCCGAGCAGTTCAAGTGAATGGAAC 194
Db 397 ACAGCTTCCTGAAGTATTTGGGCTTATGCGGCCGAGCAGTTCAAGTGAATGGAAC 338
QY 195 AGCAACACCTGAGAGGGAACACAGCAACTCAACGTCAGAGTCTCGAGTCTCAGGA 254
Db 337 AGCAACACCTGAGAGGGAACACAGCAACTCAACGTCAGAGTCTCGAGTCTCAGGA 278
QY 255 GGGAGAGGATGAGGAGCATCTGCAAGTCAAGGCCGAGCCTGAAGCTGATAGCCAGGA 314
Db 277 GGGAGAGGATGAGGAGCATCTGCAAGTCAAGGCCGAGCCTGAAGCTGATAGCCAGGA 218
QY 315 ACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGGCGAGGATGGA 374
Db 217 ACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGGCGAGGATGGA 158
QY 375 CCGCCCAATCCAGAGGAGTGAACCGCTGGAAGAGGTGAACCAATCACAGTGTTA 434
Db 157 CCGCCCAATCCAGAGGAGTGAACCGCTGGAAGAGGTGAACCAATCACAGTGTTA 98
QY 435 AAAGAAGACACGTTGAATGATGAGGCTGCTCTATGTTGGAAATTTGTTCAATAAAT 494
Db 97 AAAGAAGACACGTTGAATGATGAGGCTGCTCTATGTTGGAAATTTGTTCAATAAAT 38
QY 495 TCTCCCAATAAGCTTTACAGCCTTCTGCAAAAAA 531
Db 37 TCTCCCAATAAGCTTTACAGCCTTCTGCAAAAAA 1

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RESULT 8
AA738037/c
LOCUS
DEFINITION
  AA738037
  464 bp mRNA linear EST 22-JAN-1998
  similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ; mRNA sequence.
ACCESSION
  AA738037
VERSION
  AA738037.1 GI:2768794
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 464)
REFERENCE
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
  Emmert-Buck, M.D., Ph.D.
  cDNA Library Preparation: M. Bento Soares, Ph.D.
  DNA Sequencing by: Greg Lennon, Ph.D.
  Genome Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html
  Insert Length: 511 Std Error: 0.00
  Seq primer: -40ml3 fwd. ET from Amersham
  High quality sequence stop: 435.
  Location/Qualifiers
    1..464
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:1256204"
    /tissue_type="pooled germ cell tumors"
    /lab_host="DH10B"
    /clone_lib="NCI_CGAP GC3"
    /note="Vector: pT7T3D-Pac (Pharmacia) with a modified

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polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

## ORIGIN

```

Query Match      82.0%; Score 442; DB 9; Length 464;
Best Local Similarity 97.8%; Pred. No. 6.5e-80;
Matches 448; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 82 ATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGGCGCTATGTACAGCT 141
Db 464 ATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTAGTCCAGACGCTATGTACAGCT 405
QY 142 CCTGAAGTGAATGGGCTTATGCGGCCGAGCAGTTCAGTGAATGGAACCAACGACACA 201
Db 404 CCTGAATGATTTGGGCTTATGCGGCCGAGCAGTTCAGTGAATGGAACCAACGACACA 345
QY 202 CCTGAAGAGGGGAACCAACGACCACTCAACGTCAGGATCTCGAGTCTCAGGAGGAGAG 261
Db 344 CCTGAAGAGGGGAACCAACGACCACTCAACGTCAGGATCTCGAGTCTCAGGAGGAGAG 285
QY 262 GATGAGGAGGAGCATCTGCAAGTCAAGGCCGAGCCTGAAGCTGATGCCAGGAACAGGGT 321
Db 284 GATGAGGAGGAGCATCTGCAAGTCAAGGCCGAGCCTGAAGCTGATGCCAGGAACAGGGT 225
QY 322 CACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGGAGGAGTGGACCCGCCA 381
Db 224 CACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGGAGGAGTGGACCCGCCA 165
QY 382 AATCCAGAGGAGTGAACCGCTGGAAGAGTCAAGCAATCACAGTGTATAAAGAGAG 441
Db 164 AATCCAGAGGAGTGAACCGCTGGAAGAGTCAAGCAATCACAGTGTATAAAGAGAG 105
QY 442 ACAGTTTGAATGATGAGGAGTGTCTCTATGTTGGAAATTTGTTCAATAAATTTCTCCA 501
Db 104 GCAGTTTGAATGATGAGGAGTGTCTCTATGTTGGAAATTTGTTCAATAAATTTCTCCA 45
QY 502 ATAAAGCTTTACAGCCTTCTGCAAAAAA 539
Db 44 ATAAGAGTTTACAGCCTTCTGCAAAAAA 7

RESULT 9
AI381509/c
LOCUS
DEFINITION
  AI381509
  447 bp mRNA linear EST 28-MAR-1999
  te76b07.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
  IMAGE:2092597 3' Similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;
  mRNA sequence.
ACCESSION
  AI381509
VERSION
  AI381509.1 GI:4194290
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 447)
REFERENCE
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  This clone is available royalty-free through LLNL ; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  Insert Length: 497 Std Error: 0.00
  Seq primer: -40UP from Gibco.
  Location/Qualifiers
    1..447
    /organism="Homo sapiens"

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 505)  
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.  
21c Frontier Korean EST Project 2001  
Unpublished (2002)  
Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 8 row: B column: 09  
High quality sequence stop: 505.

Location/Qualifiers

1. 505  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="L8SCK0-8-B09"  
/sex="M"  
/cell\_line="SCK"  
/lab\_host="Top10P"  
/clone\_lib="L8SCK0"  
/note="Organ: Liver; Vector: pT7T3-Pac; Site 1: EcoRI; Site 2: NotI; The library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cell culture."

## FEATURES

source

1. 505  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="L8SCK0-8-B09"  
/sex="M"  
/cell\_line="SCK"  
/lab\_host="Top10P"  
/clone\_lib="L8SCK0"  
/note="Organ: Liver; Vector: pT7T3-Pac; Site 1: EcoRI; Site 2: NotI; The library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cell culture."

## ORIGIN

Query Match 80.9%; Score 436; DB 14; Length 505;  
Best Local Similarity 97.8%; Pred. No. 1.1e-78;  
Matches 442; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
QY 30 GTTCCTCGCTCGGACTCTTTTCCCTACTGAGATCATCTCTGTGGAATATGAGTTG 89  
Db 19 GTTCCTCGCTCGGACTCTTTTCCCTACTGAGATCATCTCTGTGGAATATGAGTTG 78  
QY 90 GCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGCGCTATGTACAGCTCTCTGAAGT 149  
Db 79 GCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGCGCTATGTACAGCTCTCTGAAT 138  
QY 150 GATTGGCCCTATGGGCGCCGAGCGATTTCAGTGATGAAGTGAACACGACACCTGAAGA 209  
Db 139 GATTGGCCCTATGGGCGCCGAGCGATTTCAGTGATGAAGTGAACACGACACCTGAAGA 198  
QY 210 AGGGGAACCAAGCAACTCAAGCTCAGGATCTTGCAGCTGCTCAGGAGGAGAGATGAGGG 269  
Db 199 AGGGGAACCAAGCAACTCAAGCTCAGGATCTTGCAGCTGCTCAGGAGGAGAGATGAGGG 258  
QY 270 AGCATCTGAGGTCAGAGGCGGAGCCTGAAGCTGATAGCCAGGAACAGGGTCAACCCACA 329  
Db 259 AGCATCTGAGGTCAGAGGCGGAGCCTGAAGCTGATAGCCAGGAACAGGGTCAACCCACA 318  
QY 330 GACTGGGTGTGAGTGAAGATGGTCTGATGGCAGGAGGTGACCGGCCAATTCAGA 389  
Db 319 GACTGGGTGTGAGTGAAGATGGTCTGATGGCAGGAGGTGACCGGCCAATTCAGA 378  
QY 390 GGAGGTGAAAACCGCTCAAGAGGTGAAAAGCAATCAAGTGTGTTAAAGAGACACCTTG 449  
Db 379 GGAGGTGAAAACCGCTCAAGAGGTGAAAAGCAATCAAGTGTGTTAAAGAGACATCTGT 438  
QY 450 AAATGATGAGGCTGCTCTTATGTTGAAATT 481  
Db 439 AAATGTTGCAGGCTGCTCTTATGTTGAAACT 470

RESULT 12

AA760996/c

LOCUS

AA760996 450 bp mRNA linear EST 26-JAN-1998  
nx32t08.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1257855 3',  
similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ; mRNA sequence.

ACCESSION

AA760996

VERSION

AA760996.1

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 450)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40m13 fwd. RT from Amersham

High quality sequence stop: 331.

Location/Qualifiers

1. 450

/organism="Homo sapiens"

/mol\_type="mRNA"

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/clone="IMAGE:1257855"

/tissue\_type="pooled germ cell tumors"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP GC4"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; 1st strand cDNA was prepared from 3 pooled

germ cell tumors, and was then primed with a Not I -

oligo(dT) primer. Double-stranded cDNA was ligated to Eco

RI adaptors (Pharmacia), digested with Not I and cloned

into the Not I and Eco RI sites of the modified pT7T3

vector. Library is normalized. Library was constructed by

Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 80.4%; Score 433.2; DB 9; Length 450;

Best Local Similarity 98.9%; Pred. No. 4e-78;

Matches 446; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 82 ATGAGTTGGCGAGGAAGATCGACTATTATTGGCTAGACCAAGGCGCTATGTACAGCT 141

Db 450 ATGAGTTGGCGAGGAAGATCGACTATTATTGGCTAGACCAAGGCGCTATGTACAGCT 391

QY 142 CCTGAAGTATTGGGCTATCGGCGCCGAGCAGTTTCAGTGATGAAGTGAACCAAGCAACA 201

Db 390 CCTGAAGTATTGGGCTATCGGCGCCGAGCAGTTTCAGTGATGAAGTGAACCAAGCAACA 331

QY 202 CCTGAAGAGAGGGAACAGCAACTCAACGTTCAGGATCCTCAGTCTCAGGAGGAGAG 261

Db 330 CCTGAAGAGAGGGAACAGCAACTCAACGTTCAGGATCCTCAGTCTCAGGAGGAGAG 271

QY 262 GATGAGGAGCATCTCGCAGTCAAGGCGCGAAGCCTCAAGCTGATACCCAGGAAACAGGGT 321

Db 270 GATGAGGAGCATCTCGCAGTCAAGGCGCGAAGCCTCAAGCTGATACCCAGGAAACAGGGT 211

QY 322 CACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTTGATGGCAGGAGGTGGACCCGCCA 381

Db 210 CACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTTGATGGCAGGAGGTGGACCCGCCA 151

QY 382 AATCCAGAGAGGTGAAAACGCTGAGAGGTGAAAAGCAATCACAGTGTGTAAGAGAG 441



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Db      150  AATCCAGAGGAGGTGAARACGCTGAAGAGCTGAAAGCAATCAACAGTGTAAAGAG 91
QY      442  ACACGTTGAATGATGCGAGGCTGCTTCATGTTGAAATTTGTTTAAATTTCTCCCA 501
Db      90  ACACGTTGAATGATGCGAGGCTGCTTCATGTTGAAATTTGTTTAAATTTCTCCCA 31
QY      502  ATAAAGCTTTACAGCTTCTGCAAAAAAAA 532
Db      30  ATAAAG-TTACAGCTTCTGCAAAAAAAA 1

RESULT 13
LOCUS   A1187350/c
DEFINITION  qf29a05.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1751408
            3' similar to SW:GGE4_HUMAN Q13068 GAGE-4 PROTEIN. [1] ;, mRNA
ACCESSION  A1187350
VERSION    A1187350.1 GI:3737988
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 455)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-re@mail.nih.gov
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 504 Std Error: 0.00
            Seq primer: -400P from Gibco
            High quality sequence stop: 391.
            Location/Qualifiers
FEATURES             source
     1..455
     /organism="Homo sapiens"
     /mol_type="mRNA"
     /db_xref="taxon:9606"
     /clone="IMAGE:1751408"
     /sex="male"
     /lab_host="DH10B"
     /clone_lib="Soares testis NHT"
     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
     polylinker; Site_1: Not 1; Site 2: Eco RI; 1st strand cDNA
     was prepared from mRNA obtained from Clontech
     Laboratories, Inc., and primed with a Not I - oligo(dT)
     primer [5].
     TGTACCATCTGAAGTGGAGCGCGCCCAATTTTCTTTTCTTTT 3'].
     Double-stranded cDNA was ligated to Eco RI adaptors
     (Pharmacia), digested with Not I and cloned into the Not I
     and Eco RI sites of the modified pT7T3 vector. Library
     went through one round of normalization to Cot5, and was
     constructed by Bento Soares and M. Fatima Bonaldo. "

Query Match      77.7%; Score 418.6; DB 9; Length 455;
Best Local Similarity 97.6%; Pred. No. 3.8e-75;
Matches 446; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

QY      82  ATGAGTTGCGAGGAGATCGACCTATTATTGGCTAGACCAAGGCGCTATGTACAGCT 141
Db      455  ATGAGTTGCGAGGAGAGTGAACCTATTATTGGCTTAGA-CAAGGCGCTATGT-CAGCT 398
QY      142  CCTGAAGTGATTGGGCTATGGCGCCGAGCAGTTCAGTGATGAAGTGAACCAAGCAACA 201

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Db      397  CTTGAATGATTGGGCTTATGGGCGCGAGCAGTTTCAGTGATGAAGTGAACCAAGCAACA 338
QY      202  CTTGAAGAAGGGGAACCGAGCAACTCAAGCTCAGGATCTCTGCAGCTGCTCAGAGGAGAG 261
Db      337  CTTGAAGAAGGGGAACCGAGCAACTCAAGCTCAGGATCTCTGCAGCTGCTCAGGAGGAGAG 278
QY      262  GATGAGGGAGCATCTGCAGGTCACAGGGCCGAGCCTGAAGCTGAAGCTGATACAGCAACAGGCT 321
Db      277  GATGAGGGAGCATCTGCAGGTCACAGGGCCGAGCCTGAAGCTCATAGCCAGAAACAGGCT 218
QY      322  CACCCACAGACTGGGCTGTGAGTGTGAAGATGGTCTCTGATGGCAGAGGTGGACCGCCA 381
Db      217  CACCCACAGACTGGGCTGTGAGTGTGAAGATGGTCTCTGATGGCAGAGATGCACCGCCA 158
QY      382  AATCCAGAGGAGGTGAAGAACGCTGAAGAGGTGAAAAGCAATCAAGTGTAAAGAAAG 441
Db      157  AATCCAGAGGAGGTGAAGAACGCTGAAGAGGTGAAAAGCAATCCAGTGTGTAAAGAAAG 98
QY      442  ACACGTTGAAATGATGACAGGCTGCTCCTATGTTTGAATTTGTTTCAATAAATTTCTCCCA 501
Db      97  ACACGTTGAAATGATGACAGGCTGCTCCTATGTTTGAATTTGTTTCAATAAATTTCTCCCA 38
QY      502  ATAAAGCTTTACAGCTTCTGCAAAAAAAA 538
Db      37  ATAAAGCTTTCAGGCTTCTGCAAAAAAAA 1

RESULT 14
LOCUS   AW016546/c
DEFINITION  UI-H-B10p-abg-g-06-0-UI.s1 NCI_CGAP_Sub2 Homo sapiens CDNA clone
            IMAGE:2711986 3', mRNA sequence.
ACCESSION  AW016546
VERSION    AW016546.1 GI:5865303
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 418)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-re@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            NCI-CGAP clone distribution information can be found through the
            I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward
            POLYA=Yes.
            Location/Qualifiers
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     /mol_type="mRNA"
     /db_xref="taxon:9606"
     /clone="IMAGE:2711986"
     /lab_host="DH10B (Life Technologies)"
     /clone_lib="NCI_CGAP_Sub2"
     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
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     NCI_CGAP Sub2 library is a subtracted library derived from
     BL-BI constitutes a mixture of 21 normalized or
     subtracted NCI_CGAP libraries: NCI_CGAP_Co4,
     NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10,
     NCI_CGAP_Co16, NCI_CGAP_Kid5, NCI_CGAP_Kid12,
     NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lym2,
     NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_CLL1, NCI_CGAP_Lei2,
     NCI_CGAP_Brn23, NCI_CGAP_Lu5, NCI_CGAP_Lu24,

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NCI\_CGAP\_Lu19, NCI\_CGAP\_GC4, NCI\_CGAP\_GC6, NCI\_CGAP\_Brn25.  
These 21 libraries were pooled and a single-stranded DNA  
preparation of the resulting mixture was used as a tracer  
in a subtractive hybridization with a driver whose  
composition is detailed below: NCI\_CGAP\_Kid3 pool 1 LLAM  
3334-3337, 3682-3683, 3798-3803 (IMAGE Clonids  
132376-132311, 1456008-1456775, 1500552-1502855)  
NCI\_CGAP\_Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778  
(IMAGE Clonids 1323912-1325831, 1471368-1472903,  
1492104-1493255) NCI\_CGAP\_Lu5 pool 1 LLAM 3575-3582,  
3851-3854 (IMAGE Clonids 1414920-1417991,  
1520904-1522439) NCI\_CGAP\_GC4 pool 1 LLAM 3164-3167,  
3716-3720, 3733-3735 (IMAGE Clonids 1257096-1258631,  
1469064-1470983, 1475592-1476743) NCI\_CGAP\_Pr22 pool 1  
LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonids  
985608-986759, 1101192-1101959, 1217928-1220615)  
NCI\_CGAP\_Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE  
Clonids 1057416-1061255, 1144584-1145351) The resulting  
subtracted library contained 4 million recombinants.  
Subtraction was performed as previously described  
[Bonaldo, Lennon & Soares (1996): Normalization and  
Subtraction: Two Approaches To Facilitate Gene Discovery.  
Genome Research 6, 791-806.  
TAG\_TISSUE=germ cell  
TAG\_LIB=NCI\_CGAP\_GC4  
TAG\_SEQ=AAATC"

## ORIGIN

Query Match 75.3%; Score 405.8; DB 9; Length 418;  
Best Local Similarity 98.3%; Pred. No. 1.5e-72;  
Matches 410; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 123 AAGCGCTATGTACAGCTCTCTGAAGTGAATGGGCTATGGCCCGAGCAGTTCAGTGA 182  
DB 418 AAGACGTAGTAGAGCTCTCTGAATGAATGGGCTATGGCCCGAGCAGTTCAGTGA 359  
QY 183 TGAAGTGGAAACAGCAACACTGAAGAGGGGAACCACTCAACGTGAGGATCTGTC 242  
DB 358 TGAAGTGGAAACAGCAACACTGAAGAGGGGAACCACTCAACGTGAGGATCTGTC 299  
QY 243 AGCTGCTCAGGAGGAGGATGAGGAGCATCTGAGGTCAAGGGCCGAGCTGAGC 302  
DB 298 AGCTGCTCAGGAGGAGGATGAGGAGCATCTGAGGTCAAGGGCCGAGCTGAGC 239  
QY 303 TGATAGCCAGGAACAGGCTACCCACAGACTGGGTGTGAGTGTGAAGTGTCTGTATGG 362  
DB 238 TCATAGCCAGGAACAGGCTACCCACAGACTGGGTGTGAGTGTGAAGTGTCTGTATGG 179  
QY 363 GCAGGAGGTGGACCCGCCAATCCAGAGGAGGTGAACCGCTGAAGAGGTGAAAAGCA 422  
DB 178 GCAGGAGGTGGACCCGCCAATCCAGAGGAGGTGAACCGCTGAAGAGGTGAAAAGCA 119  
QY 423 ATCACAGTGTAAAGAGACAGCTGAAATGATGAGGCTGCTCTATGTTGAAATTT 482  
DB 118 ATCACAGTGTAAAGAGACAGCTGAAATGATGAGGCTGCTCTATGTTGAAATTT 59  
QY 483 GTTCATTAATAATCTCCCAATAAAGCTTTACAGCTTTCTGCAAAAAA 539  
DB 58 GTTCATTAATAATCTCCCAATAAAGCTTTACAGCTTTCTGCAAAAAA 2

RESULT 15  
AA868226/c  
LOCUS  
DEFINITION  
ak48h07.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1409245  
3' similar to SW:GGE2\_HUMAN Q13066 GAGE-2 PROTEIN. [1]; mRNA  
sequence.  
AA868226  
AA868226.1 GI:2963671  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (Bases 1 to 426)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [CGAPs@mail.nih.gov](mailto:CGAPs@mail.nih.gov)  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Possible reversed clone: similarity on wrong strand  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 363.

FEATURES  
source

1..426  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1409245"  
/sex="male"  
/lab\_host="DH10B"  
/clone\_lib="Soares testis NHT"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech  
Laboratories, Inc., and primed with a Not I - oligo(dT)  
primer [5].  
TGTACCAATCTGAAGTGGAGCGCGCCCAATTTTCTTTT 3'.  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 73.7%; Score 397.2; DB 9; Length 426;  
Best Local Similarity 96.4%; Pred. No. 8.7e-71;  
Matches 405; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
QY 109 TATTGGCTAGACCAAGCGCTATGTACAGCTCTCTGAGGTGTTGGGCTATGCGGCC 168  
DB 420 TATCGGCTAGACCAAGCGCTACGTAGAGCTCTCTGAAATGNNNTTGCCTATGCGGCC 361  
QY 169 GAGCAGTTCAGTGTGAAGTGGAAACCAAGCAACCTGAAGAAGGGGAACCACTCAA 228  
DB 360 GAGCAGTTCAGTGTGAAGTGGAAACCAAGCAACCTGAAGAAGGGGAACCACTCAA 301  
QY 229 CGTCAGATCTCGAGCTGCTCAGGAGGAGAGATGAGGAGCATCTGAGGTCAAGGG 289  
DB 300 CGTCAGATCTCGAGCTGCTCAGGAGGAGAGATGAGGAGCATCTGAGGTCAAGGG 241  
QY 289 CCGAAGCTCAAGCTGATAGCAGGACAGGCTCACCCACAGACTGGGTGTGAGTGTAA 348  
DB 240 CCGAAGCTCAAGCTGATAGCAGGACAGGCTCACCCACAGACTGGGTGTGAGTGTAA 181  
QY 349 GATGGTCTCATGGGAGGAGTGGACCCGCCAAATCCAGAGGAGTGAAGAGCGCTGAA 408  
DB 180 GATGGTCTCATGGGAGGAGTGGACCCGCCAAATCCAGAGGAGTGAAGAGCGCTGAA 121  
QY 409 GAAGGTGAAGCAATCAGTGTAAAGAACACAGCTTGAATGATGAGGTGTCTCC 468  
DB 120 GAAGGTGAAGCAATCAGTGTAAAGAACAGCTTGAATGATGAGGTGTCTCC 61  
QY 469 TATGTTGAAATTTGTTTCAATTAATAATCTCCCAATAAAGCTTTACAGCTTTCTCAAAA 528  
DB 60 TATGTTGAAATTTGTTTCAATTAATAATCTCCCAATAAAGCTTTACAGCTTTCTCAAAA 1

Search completed: August 7, 2004, 13:28:48  
Job time : 2513 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2004, 08:42:53 ; Search time 390 Seconds

(without alignments)  
5871.228 Million cell updates/sec

Title: US-09-782-745-18

Perfect score: 539

Sequence: 1 GCCAGGAGCTGTGAGGCAG.....CTGCAAAAAAAAAAAAAA 539

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 5022056

Minimum DB seq length: 0

Maximum DB seq length: 539

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq 26Jan04: \*  
1: geneseqn1980s: \*  
2: geneseqn1990s: \*  
3: geneseqn2000s: \*  
4: geneseqn2001as: \*  
5: geneseqn2001bs: \*  
6: geneseqn2002as: \*  
7: geneseqn2003as: \*  
8: geneseqn2003bs: \*  
9: geneseqn2003cs: \*  
10: geneseqn2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	529.4	98.2	539	2	Aav18721 cDNA enco
2	527.2	97.8	532	2	Aax90522 GAGE-5 tu
3	527	97.8	527	7	Acc51027 Human bla
4	527	97.8	527	7	Abx76236 Lung canc
5	522.2	96.9	528	6	AbL66323 lung canc
6	519.2	96.3	532	2	Aav18720 cDNA enco
7	510.2	94.7	538	2	Aax90519 GAGE-2 tu
8	504	93.5	526	7	ADAI15802 Human GAG
9	502.8	93.3	528	7	ADAI15801 Human GAG
10	502.2	93.2	530	7	ABZ220463 GAGE-2 fu
11	468.4	86.9	535	2	Aav18717 cDNA enco
12	356.2	66.1	430	3	AAC02129 Human sec
13	303	56.2	530	4	AAS60104 Human can
14	300.8	55.8	365	4	AAS60496 Human can
15	244	45.3	277	7	ABZ19551 Group III
16	242.4	45.0	257	7	ABZ19955 Group III
17	242.4	45.0	264	7	ABZ19755 Group III
18	227.4	42.2	229	7	ABZ20437 TFS1 subc
19	227	42.1	227	7	ABZ20480 TFS1 subc
20	226	41.9	229	7	ABZ18686 Group III
21	218.4	40.5	259	7	ABZ19791 Group III
22	210	39.0	520	7	ABT15737 Human can
23	204	37.8	225	7	ABZ19533 Group III

24	202.4	37.6	509	7	ABX77605	Abx77605 Different
25	202.4	37.6	509	8	ACD42232	ACD42232 Human GAG
26	202.4	37.6	509	9	ADC24646	ADC24646 Human cDN
27	187	34.7	532	4	AAI60530	AAI60530 Human pol
28	178	33.0	219	7	ABZ19538	Abz19538 Group III
29	164.2	30.5	503	5	AAS69484	AAS69484 DNA enco
30	144.8	26.9	528	7	ABT15728	ABT15728 Human can
31	134.8	25.0	475	4	AAD14981	AAD14981 Human NOV
32	129.8	24.1	538	7	ABT15736	ABT15736 Human can
33	109.6	20.3	399	5	AAF68151	AAF68151 Human lun
34	109.6	20.3	399	6	ABK38062	ABK38062 cDNA enco
35	109.6	20.3	399	7	ACA10391	ACA10391 Human lun
36	109.6	20.3	399	7	ABX99342	ABx99342 Lung canc
37	109.6	20.3	399	10	ADE72125	Ade72125 Human lun
38	105.2	19.5	505	6	AAD24228	AAD24228 Human dif
39	105	19.5	463	6	ABA92217	ABA92217 Melanoma
40	103.2	19.1	515	4	AAH93807	AAh93807 Human pro
41	103.2	19.1	515	4	AAS63900	AAS63900 Human pro
42	103.2	19.1	515	4	AAH02872	AAh02872 Prostate
43	103.2	19.1	515	4	AAH85121	AAh85121 Human pro
44	103.2	19.1	515	5	ACA59708	ACA59708 Prostate
45	103.2	19.1	515	6	ABL95271	Ab195271 Human P10

## ALIGNMENTS

RESULT 1  
AAV18721  
ID AAV18721 standard; cDNA; 539 BP.  
AC AAV18721;  
XX  
XX  
DT 30-JUL-1998 (first entry)  
XX  
DE cDNA encoding GAGE-6 tumour rejection antigen precursor.  
XX  
KW GAGE tumour rejection antigen precursor; TRAP; tumour; diagnosis;  
KW melanoma; antigen; cytolytic T cell clone proliferation;  
KW HLA-typing assay; ss.  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 82..436  
FT /\*tag= a  
FT /transl\_except= (pos:127..129, aa:Arg)  
FT /transl\_except= (pos:196..198, aa:Ala)  
FT /transl\_except= (pos:199..201, aa:Thr)  
XX  
XX WO9749417-A1.  
FN 31-DEC-1997.  
PD  
XX  
XX 23-JUN-1997; 97WO-US010850.  
XX  
XX 24-JUN-1996; 96US-00669161.  
PR (LUDW-) LUDWIG INST CANCER RES.  
XX  
XX  
XX Debacker O, Van Den Eynde B, Boon-Falleur T;  
XX WPI; 1998-076905/07.  
DR P-PSDB; AAW47603.  
XX  
XX Isolated nucleic acid encoding GAGE tumour rejection antigen precursor -  
PT processed by HLA-Cw6 molecules into peptides, useful to diagnose  
PT melanomas.  
XX  
XX Example 13; Fig 4; 60pp; English.  
XX The present sequence encodes a GAGE-6 tumour rejection antigen  
CC precursor (TRAP). The protein is expressed in a number of tumours. In



```
RESULT 3
ACC51027
ID ACC51027 standard; cDNA; 527 BP.
XX
AC ACC51027;
XX
DT 12-JUN-2003 (first entry)
XX
DE Human bladder cancer associated cDNA sequence SEQ ID NO:144.
XX
KW Human; bladder cancer; cytostatic; gene therapy; vaccine; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003003906-A2.
XX
PD 16-JAN-2003.
XX
PF 03-JUL-2002; 2002WO-US021338.
XX
PR 03-JUL-2001; 2001US-0302814P.
XX
PR 03-AUG-2001; 2001US-0310099P.
XX
PR 08-NOV-2001; 2001US-0343705P.
XX
PR 13-NOV-2001; 2001US-0350666P.
XX
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Mack DH, Aziz N;
XX
XX WPI; 2003-201532/19.
XX
DR P-PSDB; ABR48213.
XX
PT Detecting a bladder cancer-associated transcript in a cell from a
PT patient, comprises contacting a biological sample from the patient with a
PT bladder cancer-associated polynucleotide or antibody.
XX
PS Claim 6; Page 279; 307pp; English.
XX
CC The present invention describes a method for detecting a bladder cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with a polynucleotide
CC that selectively hybridizes to a sequence that is 80 % identical to a
CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
CC encode the human bladder cancer-associated proteins given in ABR48146 to
CC ABR48242). Bladder cancer-associated sequences from the present invention
CC have cytostatic activities, and can be used in antisense gene therapy and
CC in vaccine production. The method can be used for detecting a bladder
CC cancer-associated transcript in a cell from a patient. The method is
CC useful in diagnosing or treating bladder cancer and in screening for
CC compounds that modulate bladder cancer, such as hormones or antibodies.
CC The nucleic acid molecules from the present invention may be used in
CC various screening and diagnostic methods, and for gene therapy, vaccine
CC and/or antisense/inhibition applications
XX
SQ Sequence 527 BP; 146 A; 113 C; 157 G; 111 T; 0 U; 0 Other;

Query Match          97.8%; Score 527; DB 7; Length 527;
Best Local Similarity 100.0%; Pred. No. 3.3e-138;
Matches 527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGGAGCTGTGAGGAGTGTGTGGTTCCTGCGCTCGGAGTCTTTTCTCTAC 60
Db 1 GCCAGGAGCTGTGAGGAGTGTGTGGTTCCTGCGCTCGGAGTCTTTTCTCTAC 60
QY 61 TCAGATTCACTGTGTGAATATGAGTTCGGCAGAGAGATCGACCTATTATTGGCTAGA 120
Db 61 TCAGATTCACTGTGTGAATATGAGTTCGGCAGAGAGATCGACCTATTATTGGCTAGA 120
QY 121 CCAAGGCGCTATGATCAGCCTCTGAAAGTGAATTGGGCTATCGGCCCGAGCAGTTCAGT 180
Db 121 CCAAGGCGCTATGATCAGCCTCTGAAAGTGAATTGGGCTATCGGCCCGAGCAGTTCAGT 180
```

```
QY 181 GATGAAGTGGACACGACACCTCTGAAGAGGGGACGACCACTCAACGTCAAGATCCT 240
Db 181 GATGAAGTGGACACGACACCTCTGAAGAGGGGACCACTCAACGTCAAGATCCT 240
QY 241 GCAGCTGTCTCAGGAGGGAGAGGATGAGGAGGATCTGCAGGTCACAGGCCGGAAGCCTGAA 300
Db 241 GCAGCTGTCTCAGGAGGGAGAGGATGAGGAGGATCTGCAGGTCACAGGCCGGAAGCCTGAA 300
QY 301 GTGATAGCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGAT 360
Db 301 GCTGATAGCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGAT 360
QY 361 GGGCAGGAGGTGGACCCGCCAATCCAGAGGAGGTGAAGACGCTTGAAGAGGTGAAGAG 420
Db 361 GGGCAGGAGGTGGACCCGCCAATCCAGAGGAGGTGAAGACGCTTGAAGAGGTGAAGAG 420
QY 421 CAATCACAGTGTAAAAAGAGACAGCTTGAATGATGACAGGCTGCTTATGTTGAAAT 480
Db 421 CAATCACAGTGTAAAAAGAGACAGCTTGAATGATGACAGGCTGCTTATGTTGAAAT 480
QY 481 TTGTTCAATTAATAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAAA 527
Db 481 TTGTTCAATTAATAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAAA 527

RESULT 4
ABX76236
ID ABX76236 standard; DNA; 527 BP.
XX
AC ABX76236;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polynucleotide #105.
XX
KW Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
PN WO200286443-A2.
XX
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US012476.
XX
PR 18-APR-2001; 2001US-0284770P.
XX
PR 10-MAY-2001; 2001US-0290492P.
XX
PR 09-NOV-2001; 2001US-0339245P.
XX
PR 13-NOV-2001; 2001US-0350666P.
XX
PR 29-NOV-2001; 2001US-0334370P.
XX
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX
XX WPI; 2003-093161/08.
XX
DR P-PSDB; ABU56512.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
PS Claim 22; Page 273; 453pp; English.
XX
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
```

to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the invention

SQ Sequence 527 BP; 146 A; 113 C; 157 G; 111 T; 0 U; 0 Other;

Query Match 97.8%; Score 527; DB 7; Length 527;

Best Local Similarity 100.0%; Pred. No. 3.3e-138;

Matches 527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCCAGGAGCTGTGAGCAGTGTGTGTGTTCTCGCTCCGACCTCTTTTCTCTAC 60
   |||
Db 1 GCCAGGAGCTGTGAGCAGTGTGTGTGTTCTCGCTCCGACCTCTTTTCTCTAC 60

QY 61 TGGATTCATCTGTGTAATATAGTTGGCGAGGAGATCGACTATTATGGCCTAGA 120
   |||
Db 61 TGGATTCATCTGTGTAATATAGTTGGCGAGGAGATCGACTATTATGGCCTAGA 120

QY 121 CCAAGGCGCTATGTACAGCTCTCTGAAGTGATTTGGGCTATGCGGCCGAGCAGTTCA 180
   |||
Db 121 CCAAGGCGCTATGTACAGCTCTCTGAAGTGATTTGGGCTATGCGGCCGAGCAGTTCA 180

QY 181 GATGAAGTGAACAGCAACACCTCTGAAGAGGGGAAACAGCAACTCAACGTCAGGATCCT 240
   |||
Db 181 GATGAAGTGAACAGCAACACCTCTGAAGAGGGGAAACAGCAACTCAACGTCAGGATCCT 240

QY 241 GCAGCTCTCAGGAGGAGGAGGATGAGGAGCATCTCAGTCAAGGCCGAGCCTGAA 300
   |||
Db 241 GCAGCTCTCAGGAGGAGGAGGATGAGGAGCATCTCAGTCAAGGCCGAGCCTGAA 300

QY 301 GCTGATAGCCAGGAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGAT 360
   |||
Db 301 GCTGATAGCCAGGAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGAT 360

QY 361 GGGCAGGAGTGGACCCGCCAAATCCAGAGAGTGAAACGCTCGAAGAGGTGAAAG 420
   |||
Db 361 GGGCAGGAGTGGACCCGCCAAATCCAGAGAGTGAAACGCTCGAAGAGGTGAAAG 420

QY 421 CAATCAGAGTGTAAAGAGACACGTTTGAATCATGCAGCTCTCTATGTTGGAAT 480
   |||
Db 421 CAATCAGAGTGTAAAGAGACACGTTTGAATCATGCAGCTCTCTATGTTGGAAT 480

QY 481 TTGTTCTATTAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAA 527
   |||
Db 481 TTGTTCTATTAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAA 527
```

RESULT 5

ABL66323

ID ABL66323 standard; DNA; 528 BP.

XX ABL66323;

XX 15-MAY-2002 (first entry)

XX Lung cancer related gene sequence SEQ ID NO:4660.

XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;  
XX stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;  
XX cytostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;

gene; ds.

XX Homo sapiens.

XX WO200194629-A2.

XX 13-DEC-2001.

XX 30-MAY-2001; 2001WO-US010838.

XX 05-JUN-2000; 2000US-0209473P.

XX 05-JUN-2000; 2000US-0209531P.

XX 18-SEP-2000; 2000US-0233133P.

XX 18-SEP-2000; 2000US-0233617P.

XX 20-SEP-2000; 2000US-0234009P.

XX 20-SEP-2000; 2000US-0234034P.

XX 20-SEP-2000; 2000US-0234052P.

XX 22-SEP-2000; 2000US-0234509P.

XX 22-SEP-2000; 2000US-0234567P.

XX 25-SEP-2000; 2000US-0234923P.

XX 25-SEP-2000; 2000US-0234924P.

XX 25-SEP-2000; 2000US-0235077P.

XX 25-SEP-2000; 2000US-0235082P.

XX 25-SEP-2000; 2000US-0235134P.

XX 26-SEP-2000; 2000US-0235637P.

XX 26-SEP-2000; 2000US-0235638P.

XX 27-SEP-2000; 2000US-0235711P.

XX 27-SEP-2000; 2000US-0235720P.

XX 27-SEP-2000; 2000US-0235840P.

XX 28-SEP-2000; 2000US-0235863P.

XX 28-SEP-2000; 2000US-0236028P.

XX 28-SEP-2000; 2000US-0236032P.

XX 28-SEP-2000; 2000US-0236033P.

XX 28-SEP-2000; 2000US-0236034P.

XX 28-SEP-2000; 2000US-0236109P.

XX 28-SEP-2000; 2000US-0236111P.

XX 29-SEP-2000; 2000US-0236842P.

XX 29-SEP-2000; 2000US-0236891P.

XX 02-OCT-2000; 2000US-0237172P.

XX 02-OCT-2000; 2000US-0237173P.

XX 02-OCT-2000; 2000US-0237278P.

XX 02-OCT-2000; 2000US-0237294P.

XX 02-OCT-2000; 2000US-0237295P.

XX 03-OCT-2000; 2000US-0237316P.

XX 03-OCT-2000; 2000US-0237425P.

XX 03-OCT-2000; 2000US-0237598P.

XX 03-OCT-2000; 2000US-0237604P.

XX 03-OCT-2000; 2000US-0237606P.

XX 03-OCT-2000; 2000US-0237608P.

XX 01-NOV-2000; 2000US-0244857P.

XX 01-NOV-2000; 2000US-0245084P.

XX (AVAL-) AVALON PHARM.

XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;

XX Soppet DR, Weaver Z;

XX WPI; 2002-198264/24.

XX Screening for anti-neoplastic agent involves exposing cells to a chemical

XX agent to be tested for anti-neoplastic activity, and determining a change

XX in expression of a gene of a signature gene set.

XX Claim 1; SEQ ID NO 4660; 44pp; English.

XX The present invention describes a method (M1) for screening for an anti-  
XX neoplastic agent. The method involves exposing cells to a chemical agent  
XX to be tested for anti-neoplastic activity, determining a change in  
XX expression of at least one gene (I) of a signature gene set, where (I)  
XX comprises a sequence (S) selected from 8447 sequences (given in ABL61664  
XX to ABL70110), or is at least 95% identical to (S), where a change in  
XX expression is indicative of anti-neoplastic activity. (I) has cytostatic



CC activity and can be used in gene therapy. M1 can be used for screening an  
CC anti-neoplastic agent, and can be used for producing a product which is  
CC the data collected with respect to the anti-neoplastic agent as a result  
CC of M1, and the data is sufficient to convey the chemical structure and/or  
CC properties of the agent. M1 can be used in the treatment of cancer such  
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,  
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell  
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous  
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's  
CC tumour

```

Query Match          96.9%;   Score 522.2;   DB 6;   Length 528;
Best Local Similarity 99.4%;   Pred. No. 7.5e-137;
Matches 524; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 GCCAGGAGCTGTGAGGCAGTGCTGTGTGGTTCCTGCCGTCCGGACTCTTTTTCCTCTAC 60

db  
2 GCCAGGGAGCTGTGAGGCAGTCTGTGCTTCCTCCCGACATCATTTCATCATCA

QY 61 TGAGATTTCATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGA 120

Db  
62 TGAGATTCA TCTGTGTGAAATATGAGTTGGCCGACCATCCACCTATTATTCCTCCTT

QY 121 CCAAGCGCTATGTACAGCCTCCTGAAGTGATTGGCCCTATGCGGCCGAGCAGTTTCAGT 180

Db  
122 CCAAGGGCGTATGTACAGCCCTCTGAAAATGATTGGGCGCTATCGCGCGCCCAACATTCAGCT 181

QY 181 GATGAAGTGGAAACCAGCAACACTGAAGAAGGGAAACCAGCAACTCAACGTCAGGATCCT 240

db  
182 GATGAAGTGGAAACAGCAACACTGAAGAAGGGGAACAGCAACTCAACCTCCGATCCT 247

QY 241 GCAGCTGCTCAGGAGGGAGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAAGCCTGAA 300

db 242 GCAGCTGCTCAGGAGGGAGAGGATGAGGGAGCATCTTGAGGTCAAGGGCGACCCCTCAA 301

QY 301 GCTGATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCCTGAT 360

db 302 GCTGATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTCTGAAGCTGCTCCTCAT 361

QY 361 GGGCAGGAGGTGGACCCGCCAAATCCAGAGGAGTGAAAACGCCCTGAAGAAGGTGAAAAG 420

Dbb

362 GGGCAGGAGATGGACCCGCCCAATCCAGAGGAGGTGAAAAAGCCTGAAGAAGGTGAAAAGG 421

QY 421 CAATCACAGTGTAAAGAAGACACAGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAT 480

Db  
422 CAATCACAGTGTAAAGAAGGCACGTTGAAATGATGCAGGCCTGCTCCTATGTTGGAAT 481

QY 481 TTGTTTCATTAAAAATTCTCCCAATAAAGCTTTACAGCCCTTCGCAAAA 527

Db  
482 TTGTTTCATTAAAAATTCTCCCAATAAAAGCTTTACAGCCTTCTGCAAAA 528

RESULTS 6  
AAV18720

ID AAV18720 standard; cDNA; 532 BP.  
XX

AAV18720; AC

DT 30-JUL-1998 (first entry)  
XX

DE cDNA encoding GAGE-5 tumour rejection antigen precursor.

XX	GAGE	tumour	rejection	anti-ga	prolifer	EMSA	2'-phos
XX							
KW							

melanoma; antigen; cytolytic T cell clone proliferation;  
melanoma; tumour rejection antigen precursor; IRAP; tumour; diagnosis; KW

KW HLA-typing assay; ss.  
XX

OS Homo sapiens.  
vv

xx	Key	Location/Qualifiers
FH		

ET	75.	.429	CDS
ET	1	1	ET

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Db 361 AGATGACCGCGCCAAATCCAGAGGAGGTGAAAACGCCCTGAAGAAGGTGAAAAAGCAATCAC 420  
 QY 428 AGTGTTAAAGAACACACAGTTGAAATGATCAGGCTGCTCTATGTTGGAAATTTGTTCA 487  
 Db 421 AGTGTTAAAGAACACACAGTTGAAATGATCAGGCTGCTCTATGTTGGAAATTTGTTCA 480  
 QY 488 TTAATAATTCCTCCCAATAAAGCTTTACAGCCTTTCTGCAAAAAAATAAAAAA 539  
 Db 481 TTAATAATTCCTCCCAATAAAGCTTTACAGCCTTTCTGCAAAAAAATAAAAAA 532

RESULT 7  
 AAX90519  
 ID AAX90519 standard; cdna; 538 BP.  
 XX  
 AC AAX90519;  
 XX  
 DT 30-SEP-1999 (first entry)  
 XX  
 DE GAGE-2 tumour rejection antigen clone nucleotide sequence.  
 XX  
 KW Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection;  
 KW therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;  
 KW GAGE; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09937665-A1.  
 XX  
 PD 29-JUL-1999.  
 XX  
 PF 12-JAN-1999; 99WO-US000775.  
 XX  
 PR 23-JAN-1998; 98US-00012818.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Falleur T;  
 XX WPT; 1999-469111/39.  
 DR  
 XX New isolated peptides which bind to HLA-A29 molecules, which are tumor  
 PT rejection antigens used for detection and therapy of pathological  
 PT conditions, e.g. cancer.  
 XX  
 PS Example 13; Fig 4; 62pp; English.  
 XX  
 CC The present invention describes peptides which bind to human leukocyte  
 CC antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into  
 CC tumour rejection antigens. They can be used for detecting cytolytic T  
 CC lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-  
 CC typing assays. Complexes of HLA-29 molecules and the peptides can be used  
 CC for stimulating CTLs in vivo. The present sequence represents a GAGE  
 CC tumour rejection antigen clone, from an example from the present  
 CC invention  
 XX  
 SQ Sequence 538 BP; 160 A; 116 C; 155 G; 107 T; 0 U; 0 Other;

Query Match 94.7%; Score 510.2; DB 2; Length 538;  
 Best Local Similarity 98.0%; Pred. No. 1.8e-133;  
 Matches 528; Conservative 0; Mismatches 8; Indels 3; Gaps 1;

QY 1 GCCAGGAGCTGTGTAGGAGTGCTGTGTGGTTCCTGCGCTCGGACTCTTTTCTCTAC 60  
 Db 3 GCCAGGAGCTGTAGGAGTGCTGTGTGGTTCCTGCGCTCGGACTCTTTTCTCTAC 62  
 QY 61 TGAGATTCATCTGTGTGAATATGATGTGGGAGGAAGATCGACCTATATGGCCTAGA 120  
 Db 63 TGAGATTCATCTGTGTGAATATGATGTGGGAGGAAGATCGACC--TATCGGCCTAGA 119  
 QY 121 CCAAGGCGCTATGTACAGCTCTCTGAAGTGTGGGCTATGCGGCCGAGCAGTTCAGT 180  
 Db 120 CCAAGACGCTACGTAGAGCCCTCTGAATGATGTGGGCTATGCGGCCGAGCAGTTCAGT 179

QY 181 GATGAAGTGAACCCAGCAACACCTGAAGAGGGGAAACCCAGAACTCAACCTCAGGATCCT 240  
 Db 180 GATGAAGTGAACCCAGCAACACCTGAAGAGGGGAAACCCAGAACTCAACCTCAGGATCCT 239  
 QY 241 GCAGCTGCTCAGGAGGAGGAGATGAGGAGCATCTGCAGGTCAAGGCCGAGGCTGAA 300  
 Db 240 GCAGCTGCTCAGGAGGAGGAGATGAGGAGCATCTGCAGGTCAAGGCCGAGGCTGAA 299  
 QY 301 GCTGATAGCCAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGTCCTGAT 360  
 Db 300 GCTCATAGCCAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGTCCTGAT 359  
 QY 361 GGGCAGGAGGTGACCCGCCCAATCCAGAGGAGTGAAGAGCGCTGAAGAGGTGAAAG 420  
 Db 360 GGGCAGGAGATGACCCGCCCAATCCAGAGGAGTGAAGAGCGCTGAAGAGGTGAAAG 419  
 QY 421 CAATCAGAGTTTAAAGAGACAGCTTGAATGATGACAGCTGCTCTATGTTGGAAT 480  
 Db 420 CAATCAGAGTTTAAAGAGACAGCTTGAATGATGACAGCTGCTCTATGTTGGAAT 479  
 QY 481 TTGTTTCAATAAATTCCTCCCAATAAAGCTTTACAGCCTTTGCAAAAAAATAAAAAA 539  
 Db 480 TTGTTTCAATAAATTCCTCCCAATAAAGCTTTACAGCCTTTGCAAAAAAATAAAAAA 538

RESULT 8  
 ADA15802  
 ID ADA15802 standard; cdna; 526 BP.  
 XX  
 AC ADA15802;  
 XX  
 DT 06-NOV-2003 (first entry)  
 XX  
 DE Human GAGE-7B cdna.  
 XX  
 KW Human; GAGE-7B; gene; ss; cytolytic T lymphocyte; CTL;  
 KW human leukocyte antigen; HLA; tumour rejection antigen precursor;  
 KW major histocompatibility complex; MHC; cytolytic T cell proliferation;  
 KW chromosome Xp11.2-p11.4.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 55..408  
 FT /\*Tag= a  
 FT /product= "Human GAGE-7B"  
 FT /transl\_except= (pos:115..162, aa: GPMRPEQGSDEVPEMI)  
 FT /transl\_except= (pos:265..306, aa: HPQIGKPEAHSEQ)  
 XX  
 US6509172-B1.  
 PD 21-JAN-2003.  
 XX  
 PF 30-SEP-1998; 98US-00163748.  
 XX  
 PR 30-SEP-1998; 98US-00163748.  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI De Backer O, Van Den Eynde B, Boon-Falleur T;  
 XX WPI; 2003-401119/38.  
 DR P-PSDB; ADA15777.  
 XX  
 PT New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tumor  
 PT rejection antigen precursors, which complex to major histocompatibility  
 PT complex molecules to facilitate the proliferation of cytolytic T cells.  
 XX  
 PS Claim 1; Col 9-10; 15pp; English.  
 XX  
 CC The invention relates to isolated GAGE-7B and GAGE-8 polypeptides and the  
 CC nucleic acid molecules encoding them. The invention also relates to an

CC expression vector comprising an isolated nucleic acid molecule of the  
CC invention operably linked to a promoter, a recombinant cell comprising  
CC the isolated nucleic acid molecule or the expression vector and an  
CC expression kit useful in generating cytolytic T lymphocytes (CTLs) or  
CC determining if CTLs are present in a sample comprising the isolated  
CC nucleic acid molecule and the isolated nucleic acid that encodes a human  
CC leukocyte antigen (HLA) molecule. The GAGE-7B and GAGE-8 nucleic acid  
CC molecules encode tumour rejection antigen precursors, which complex to  
CC major histocompatibility complex (MHC) molecules to facilitate the  
CC proliferation of cytolytic T cells. This sequence represents cDNA  
CC encoding the human GAGE-7B polypeptide of the invention. The gene resides  
CC on chromosome Xp11.2-p11.4.  
XX  
SQ Sequence 526 BP; 168 A; 109 C; 143 G; 106 T; 0 U; 0 Other;

Query Match 93.5%; Score 504; DB 7; Length 526;  
Best Local Similarity 99.0%; Pred. No. 1e-131;  
Matches 507; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 28 TGGTTCCTGCGGCTCTTTCTCTACTGAGATTCATCTGTGAAATATGAGT 87  
Db 1 TGGTTCCTGCGGCTCTTTCTCTACTGAGATTCATCTGTGAAATATGAGT 60  
QY 88 TGGCGAGGAAGATGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTCGAA 147  
Db 61 TGGCGAGGAAGATGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTCGAA 120  
QY 148 GTGATTGGGCTATGCGGCGGAGCAGTTCATGATGAAGTGGAAACCAACCTGAA 207  
Db 121 ATGATTGGGCTATGCGGCGGAGCAGTTCATGATGAAGTGGAAACCAACCTGAA 180  
QY 208 GAAGGGGAACCAAGCACTCAAGTTCAGGATCTGCGAGTCTCAGAGGGAGGATGAG 267  
Db 191 GAAGGGGAACCAAGCACTCAAGTTCAGGATCTGCGAGTCTCAGAGGGAGGATGAG 240  
QY 268 GGAGCATCTGCAGGTCAAGGGCCGAGGCTGAAGCTGATAGCCAGGAACAGGGTCAACCA 327  
Db 241 GGAGCATCTGCAGGTCAAGGGCCGAGGCTGAAGCTCATAGCCAGGAACAGGGTCAACCA 300  
QY 328 CAGACTGGGTGTGATGTGAAGATGGTCTGATGGCGAGGAGTGGACCCGCCAATCA 387  
Db 301 CAGACTGGGTGTGATGTGAAGATGGTCTGATGGCGAGGAGTGGACCCGCCAATCA 360  
QY 388 GAGGAGTGAACCCCTGGAAGAGGTGAAGCAATCACAGTGTAAAGAGACAGT 447  
Db 361 GAGGAGTGAACCCCTGGAAGAGGTGAAGCAATCACAGTGTAAAGAGACAGT 420  
QY 448 TGAATGATGACGGCTGCTCCTATTTTGAATTTTGTTCATTAAATTTCTCCCAATAAG 507  
Db 421 TGAATGATGACGGCTGCTCCTATGTGTGAAATTTTGTTCATTAAATTTCTCCCAATAAG 480  
QY 508 CTTTACAGCTTCTGCAAAAAAATAAAAAA 539  
Db 481 CTTTACAGCTTCTGCAAAAAAATAAAAAA 512

RESULT 9  
ADA15801  
ID ADA15801 standard; cDNA; 528 BP.  
XX  
AC ADA15801;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
DE Human GAGE-8 cDNA.  
XX  
KW Human; GAGE-8; gene; ss; cytolytic T lymphocyte; CTL;  
KW human leukocyte antigen; HLA; tumour rejection antigen precursor;  
KW major histocompatibility complex; MHC; cytolytic T cell proliferation;  
XX chromosome Xp11.2-p11.4.  
OS Homo sapiens.  
XX

PH Key Location/Qualifiers  
FT CDS 73..423  
FT /\*tag= a  
FT /product= "Human GAGE-8"  
FT /transl\_except= {pos:244..246, aa:Gln}  
FT /transl\_except= {pos:400..402, aa:Lys}  
XX  
FN US6509172-B1.  
XX  
XX  
PD 21-JAN-2003.  
XX  
XX  
PF 30-SEP-1998; 98US-00163748.  
XX  
XX  
PR 30-SEP-1998; 98US-00163748.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
XX  
PI De Backer O, Van Den Eynde B, Boon-Falleur T;  
XX  
DR WPI; 2003-401119/38.  
DR P-PSDB; ADA15778.  
XX  
PT New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tumor  
PT rejection antigen precursors, which complex to major histocompatibility  
PT complex molecules to facilitate the proliferation of cytolytic T cells.  
XX  
PS Claim 1; Col 7-10; 15pp; English.  
XX  
CC The invention relates to isolated GAGE-7B and GAGE-8 polypeptides and the  
CC nucleic acid molecules encoding them. The invention also relates to an  
CC expression vector comprising an isolated nucleic acid molecule of the  
CC invention operably linked to a promoter, a recombinant cell comprising  
CC the isolated nucleic acid molecule or the expression vector and an  
CC expression kit useful in generating cytolytic T lymphocytes (CTLs) or  
CC determining if CTLs are present in a sample comprising the isolated  
CC nucleic acid molecule and the isolated nucleic acid that encodes a human  
CC leukocyte antigen (HLA) molecule. The GAGE-7B and GAGE-8 nucleic acid  
CC molecules encode tumour rejection antigen precursors, which complex to  
CC major histocompatibility complex (MHC) molecules to facilitate the  
CC proliferation of cytolytic T cells. This sequence represents cDNA  
CC encoding the human GAGE-8 polypeptide of the invention. The gene resides  
CC on chromosome Xp11.2-p11.4.  
XX  
SQ Sequence 528 BP; 158 A; 112 C; 151 G; 107 T; 0 U; 0 Other;

Query Match 93.3%; Score 502.8; DB 7; Length 528;  
Best Local Similarity 98.1%; Pred. No. 2.2e-131;  
Matches 520; Conservative 0; Mismatches 7; Indels 3; Gaps 1;  
QY 10 CTGTGAGGCGAGTGTGTGTCTCTGCGCTCCGAGCTCTTTTCTCTACTGAGATTCA 69  
Db 1 CTGTGAGGCGAGTGTGTGTCTCTGCGCTCCGAGCTCTTTTCTCTACTGAGATTCA 60  
QY 70 TCTGTGTGAATATGAGTTGGCGAGGAGATCGACCTATTATTGGCCCTAGACCAAGCGC 129  
Db 61 TCTGTGTGAATATGAGTTGGCGAGGAGATCGACCTATTATTGGCCCTAGACCAAGCGC 117  
QY 130 TATGTACAGCTCTCTGAAGTGAATTTGGGCTATGCGGCCGAGAGTTCAGTGAAGATG 189  
Db 118 TACGTAGAGCTCTCTGAATATGATTGGGCTATGCGGCCGAGAGTTCAGTGAAGATG 177  
QY 190 GAACCAAGCAACCTGAGAGAGGGGMAACCAAGCACTCAACCTCAGGATCTCTGAGCTCT 249  
Db 178 GAACCAAGCAACCTGAGAGAGGGGMAACCAAGCACTCAACCTCAGGATCTCTGAGCTCT 237  
QY 250 CAGGAGGAGAGGATGAGGAGAGCATCTGAGGTCAAGGGCCGAGAGCTGAAGCTGATAGC 309  
Db 238 CAGGAGGAGAGGATGAGGAGAGCATCTGAGGTCAAGGGCCGAGAGCTGAAGCTGATAGC 297  
QY 310 CAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGTATGGGAGG 369  
Db 298 CAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGTATGGGAGG 357

QY 370 GTGGACCCGCCAAATCCAGAGGAGTGAACCCCTGAAGAGGTGAAAGCAATCACAG 429  
 Db 358 ATGGACCCGCCAAATCCAGAGGAGTGAACCCCTGAAGAGGTGAAAGCAATCACAG 417  
 QY 430 TGTAAAGAGACACAGTTGAAATGATGAGGCTGCTCTATGTTGAAATTTGTCATT 489  
 Db 418 TGTAAAGAGACACAGTTGAAATGATGAGGCTGCTCTATGTTGAAATTTGTCATT 477  
 QY 490 ARAATTCTCCCAATAAGCTTTACAGCCTTCTGCAAAAAAAGAAAAA 539  
 Db 478 AAAATTCTCCCAATAAGCTTTACAGCCTTCTGCAAAAAAAGAAAAA 527

RESULT 10  
 ABZ20463  
 ID ABZ20463 standard; cDNA; 530 BP.  
 XX  
 AC ABZ20463;  
 XX  
 DT 23-JAN-2003 (first entry)  
 XX  
 DE GAGE-2 full length cDNA sequence SEQ ID NO:2890.  
 XX  
 KW Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;  
 KW immune response; virology; immunology; microbiology; molecular biology;  
 KW recombinant DNA technology; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200278516-A2.  
 PD  
 PD 10-OCT-2002.  
 XX  
 XX 28-MAR-2002; 2002WO-US010421.  
 XX  
 PR 30-MAR-2001; 2001US-0280255P.  
 PR 28-AUG-2001; 2001US-0315563P.  
 PR 09-JAN-2002; 2002US-0347313P.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Wang T, Wang S, Bangur CS, Gaiger A;  
 XX  
 DR WPI; 2003-058387/05.  
 DR P-PSDB; ABP54447.  
 XX  
 PT New immunogenic polynucleotides or polypeptides useful for diagnosing,  
 PT preventing and treating cancer expressing CT or CP mRNA antigens, and in  
 PT virology, immunology, microbiology, molecular biology and recombinant DNA  
 PT techniques.  
 XX  
 PS Claim 1; SEQ ID NO 2890; 207pp; English.  
 XX  
 CC ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and  
 CC ABP54446 to ABP54472 represent protein (II) sequences, from the present  
 CC invention. (I) and (II) have cytostatic activity and can be used in gene  
 CC therapy and vaccines. (I), (II), antibodies and compositions from the  
 CC present invention are useful for diagnosing, preventing and treating  
 CC cancer, which expresses CT or CP mRNA antigens. They are useful for  
 CC stimulating immune response. They can also be useful in virology,  
 CC immunology, microbiology, molecular biology and recombinant DNA  
 CC techniques. N.B. The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 530 BP; 152 A; 116 C; 155 G; 107 T; 0 U; 0 Other;

Query Match 93.2%; Score 502.2; DB 7; Length 530;  
 Best Local Similarity 97.9%; Pred. No. 3.3e-131;  
 Matches 520; Conservative 0; Mismatches 8; Indels 3; Gaps 1;  
 QY 1 GCACAGGAGTGTGAGGAGTGTGTGTTCTCTGCGGACTCTTTTCTCTAC 60  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 3 GCACAGGAGTGTGAGGAGTGTGTGTGTTCTCTGCGGACTCTTTTCTCTAC 62  
 QY 61 TGAGATTTCATCTGTGTGAATATAGTTGCGAGGAGATCGACCTATTATTGGCCCTAGA 120  
 Db 63 TGAGATTTCATCTGTGTGAATATAGTTGCGAGGAGATCGACCTATTATTGGCCCTAGA 119  
 QY 121 CCAAGGCGCTATGTACAGCCTCTGAAAGTGATTGGGCTTATGCGGCCCGAGCAGTTTCAGT 180  
 Db 120 CCAAGGCGCTATGTACAGCCTCTGAAATGATTGGGCTTATGCGGCCCGAGCAGTTTCAGT 179  
 QY 181 GATGAAGTGGAAACCAAGCAACCTGAAAGAGGGAACCAAGCAACCTGAAAGTTCCT 240  
 Db 180 GATGAAGTGGAAACCAAGCAACCTGAAAGAGGGAACCAAGCAACCTGAAAGTTCCT 239  
 QY 241 GCAGCTGCTCAGAGGAGGAGGAGGAGGAGCATCTGCAGGTCAAGGGCCGAGGCTGAA 300  
 Db 240 GCAGCTGCTCAGAGGAGGAGGAGGAGGAGCATCTGCAGGTCAAGGGCCGAGGCTGAA 299  
 QY 301 GCTGATAGCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGAT 360  
 Db 300 GCTCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGAT 359  
 QY 361 GGCAGGAGGTGACCCGCCAAATCCAGAGGAGTGAACCGCTGAAAGTGAAG 420  
 Db 360 GGCAGGAGGTGACCCGCCAAATCCAGAGGAGTGAACCGCTGAAAGTGAAG 419  
 QY 421 CAATCACAGTGTAAAGAGACACGTTGAAATGATGACAGGCTGCTCTATGTTGAAAT 480  
 Db 420 CAATCACAGTGTAAAGAGACACGTTGAAATGATGACAGGCTGCTCTATGTTGAAAT 479  
 QY 481 TTGTTCAATTAATAATCTCCCAATAAGCTTTACAGCCTTTGCAAAAAA 531  
 Db 480 TTGTTCAATTAATAATCTCCCAATAAGCTTTACAGCCTTTGCAAAAAA 530

RESULT 11  
 AAV18717  
 ID AAV18717 standard; cDNA; 535 BP.  
 XX  
 AC AAV18717;  
 XX  
 DT 30-JUL-1998 (first entry)  
 XX  
 DE CDNA encoding GAGE-2 tumour rejection antigen precursor.  
 XX  
 KW GAGE tumour rejection antigen precursor; TRAP; tumour; diagnosis;  
 KW melanoma; antigen; cytolytic T cell clone proliferation;  
 KW HLA-typing assay; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 81..431  
 FT /\*tag= a  
 FT /transl\_except= (pos:192..194, aa:Ala)  
 FT /transl\_except= (pos:195..197, aa:Thr)  
 XX  
 PN WO9749417-A1.  
 XX  
 PD 31-DEC-1997.  
 XX  
 PF 23-JUN-1997; 97WO-US010850.  
 XX  
 PR 24-JUN-1996; 96US-00669161.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Debacker O, Van Den Eynde B, Boon-Falleur T;  
 XX  
 DR WPI; 1998-076905/07.  
 DR P-PSDB; AAW47599.  
 XX  
 PT Isolated nucleic acid encoding GAGE tumour rejection antigen precursor -

processed by HLA-Cw6 molecules into peptides, useful to diagnose melanomas.

Example 13; Fig 4; 60pp; English.

The present sequence encodes a GAGE-2 tumour rejection antigen precursor (TRAP). The protein is expressed in a number of tumours. In contrast the only normal tissue which expresses GAGE TRAP protein is testis. Several GAGE TRAPs have been identified (see AAV18717-21). The major difference between these proteins and GAGE-1 (AAV05540) is the absence of a stretch of 143 bases located at position 379 to 521 of the GAGE-1 TRAP sequence. The rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5' end is totally different from the other GAGE cDNAs for the first 112 bases. This region of GAGE-3 cDNA contains a long repeat and a hairpin structure. The antigens can be used to diagnose melanomas, characterised by expression of a TRAP or presentation of a tumour rejection antigen. Antigens shed into blood or urine can be observed and then used to confirm a diagnosis of melanoma using cytolytic T cell clone proliferation methodologies. Other uses for the processed peptides, include HLA-typing assays for, e.g. skin graft or organ transplants

Sequence 535 BP; 158 A; 112 C; 156 G; 109 T; 0 U; 0 Other;

Query Match 86.9%; Score 468.4; DB 2; Length 535;  
Best Local Similarity 95.6%; Pred. No. 1.1e-121;  
Matches 516; Conservative 0; Mismatches 16; Indels 8; Gaps 3;

```

QY 1 GCCAGGAGCTGTGAGGAGTCTGTGTGGTTCCCTGCCCTCCGACTCTTTTTCCTC-TA 59
DB 3 GCCAGGAGCTGTGAGGAGTCTGTGTG-----TTCCTGCTCCGACTCTTTTTCCTCTTA 58
QY 60 CTGAGATTCATCTGTGTGAATATGAGTTGGGAGGAGATGACACTATTATTTGGCTAG 119
DB 59 CTGAGATTCATCTGTGTGAATATGAGTTGGGAGGAGATGACCC---TATCGCCTAG 115
QY 120 ACCAAGGCGCTATGACAGCCCTCTGAAGTATGGGCTATGCGGCCGAGCAGTTCTAG 179
DB 116 ACCAAGAGCTACGTAGAGCTCTCTGAATGATTTGGGCTATGCGGCCGAGCAGTTCTAG 175
QY 180 TGATGAAGTGAACCCAGCAGACACCTTGAGAGAGGGGAAACAGCAACTCAACGTCAGGATCC 239
DB 176 TGATGAAGTGAACCCAGAGCCCTCTCTGAAGAGGGGAAACAGCAACTCAACGTCAGGATCC 235
QY 240 TGCAGCTGCTCAGGAGGAGAGGTGAGGAGGACATCTGCAGTCAAGGCCGAGACCTTGA 299
DB 236 TGCAGCTGCTCAGGAGGAGAGGTGAGGAGGACATCTGCAGTCAAGGCCGAGACCTTGA 295
QY 300 AGCTGATAGCCAGGAAACAGGGGTACCCACAGACTGGGTGTGAGTGTGAAGTGGTCTCTGA 359
DB 296 AGCTGAGAGCCAGGAAACAGGGGTACCCACAGACTGGGTGTGAGTGTGAAGTGGTCTCTGA 355
QY 360 TGGGAGAGGTGGACCCGCGCAATTCAGAGAGGTGAAACCGCTGAGAGAGGTGAAAA 419
DB 356 TGGGAGAGGATGAGACCCGCGCAATTCAGAGAGGTGAAACCGCTGAGAGAGGTGAAAA 415
QY 420 GCAATCAGAGTGTAAAGAGACACCTTGAATGATGAGCAGCTGCTCTCTATTTGGAAA 479
DB 416 GCAATCAGAGTGTAAAGAGACATGTTGAATGATGAGCAGCTGCTCTCTATTTGGAAA 475
QY 480 TTTGTTTCATTAATAATTCCTCCCAATAAAGCTTTTACAGCCCTTCTGCAAAAAA 539
DB 476 TTTGTTTCATTAATAATTCCTCCCAATAAAGCTTTTACAGCCCTTCTGCAAAAAA 535

```

RESULT 12

AAC02129

ID AAC02129 standard; cDNA; 430 BP.

XX

AC AAC02129;

XX

DT 06-OCT-2000 (first entry)

XX

Human secreted protein 5' EST, SEQ ID NO: 2127.  
Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
gene therapy; chromosome mapping; ss.

OS Homo sapiens.

PN EP1033401-A2.

XX

PD 06-SEP-2000.

XX

PF 21-FEB-2000; 2000EP-00200610.

XX

PR 26-FEB-1999; 99US-0122487P.

XX

PA (GEST ) GENSET.

XX

PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX

DR WPI; 2000-500381/45.

XX

DR P-PSDB; AAG02123.

XX

New nucleic acid that is a 5' expressed sequence tag (5' EST) for

obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX

PS Claim 1; SEQ ID NO 2127; 71pp + Sequence Listing; English.

XX

The present sequence is one of a large number of 5' ESTs derived from  
mRNAs encoding secreted proteins. An ORF has been identified within the  
sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs  
derived from 30 different tissues. EST sequences usually correspond  
mainly to the 3' untranslated region (UTR) of the mRNA because they are  
often obtained from oligo-dT primed cDNA libraries. Such ESTs are not  
well suited for isolating cDNA sequences derived from the 5' ends of  
mRNAs and even in those cases where longer cDNA sequences have been  
obtained, the full 5' UTR is rarely included. 5' ESTs are derived from  
mRNAs with intact 5' ends and can therefore be used to obtain full length  
cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,  
gene therapy and chromosome mapping procedures. They are used to obtain  
upstream regulatory sequences and to design expression and secretion  
vectors

Sequence 430 BP; 101 A; 102 C; 134 G; 85 T; 0 U; 8 Other;

Query Match 66.1%; Score 356.2; DB 3; Length 430;

Best Local Similarity 97.3%; Pred. No. 4.1e-90;

Matches 366; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 1 GCCAGGAGCTGTGAGGAGTCTGTGTGGTTCTTGGCTCCGACTCTTTTTCCTCTAC 60

DB 56 GCCAGGAGCTGTGAGGAGTCTGTGTGGTTCTTGGCTCCGACTCTTTTTCCTCTAC 115

QY 61 TGAGATTTCATCTGTGTGAATATGAGTTGGGAGAGATGACCTATTATTGGCTAGA 120

DB 116 TGAGATTTCATCTGTGTGAATATGAGTTGGGAGAGATGACCTATTATTATTGGCTAGA 174

QY 121 CCAAGGCGCTATGTACAGCCCTCTTGAAGTGTGGCCCTATGCGGCCCGAGCAGTTCACT 180

DB 175 CCAAGGCGCTATGTACAGCCCTCTTGAAGTGTGGCCCTATGCGGCCCGAGCAGTTCACT 234

QY 181 GATGAAGTGAACCCAGCAGACACCTGAGAGAGGGGAAACAGCAACTCAACGTCAGGATCCT 240

DB 235 GATGAAGTGAACCCAGCAGACACCTGAGAGAGGGGAAACAGCAACTCAACGTCAGGATCCT 294

QY 241 GCAGTGTCTCAGGAGGAGGAGGATGAGGAGCAGTCTGCAGGTCAAGGCCGAGCCGCTGAA 300

DB 295 GCAGTGTCTCAGGAGGAGGAGGATGAGGAGCAGTCTGCAGGTCAAGGCCGAGCCGCTGAA 354

QY 301 GCTGATAGCCAGGAAACAGGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTTGAT 360

DB 355 GCTGATAGCCAGGAAACAGGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTTGAT 414

```
QY 361 GGGCAGGAGGTGGACC 376
Db 415 GGGCAGGAGATGGMC 430

RESULT 13
AAS60104/c
ID AAS60104 standard; cDNA; 530 BP.
XX
AC AAS60104;
XX
XX 29-JAN-2002 (first entry)
DT
XX
DE Human cancer agent-sensitive marker #105.
XX
XX Human; cancer cell marker; TAXOL; cytostatic; tumour; carcinoma;
KW squamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia;
KW lymphocytic leukaemia; lymphoma; plasmocytoma; reticulum cell sarcoma;
KW Hodgkin's disease; glioma; ss.
XX
OS Homo sapiens.
XX
XX WO200179556-A2.
XX
XX 25-OCT-2001.
XX
XX 13-APR-2001; 2001WO-US012132.
XX
XX 14-APR-2000; 2000US-0197538P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lillie J, Brown JL, Bolt A, Van Huffel C;
XX
XX WPI; 2001-602933/68.
XX
XX Novel nucleic acid, used as a marker to determine the effectiveness of
PT using TAXOL to treat cancer cell growth in individuals.
XX
XX Claim 1; Page 120; 527pp; English.
XX
XX The invention relates to 1046 novel nucleic acids which are used as
CC markers for determining the sensitivity of a cancer cell to the
CC anticancer agent TAXOL. Cancer cells can be treated with TAXOL when they
CC are shown to express one of the 242 sensitivity markers or the cells are
CC shown not to express one of the 804 resistance markers. The methods can
CC be used to determine the effectiveness of TAXOL in the treatment of
CC cancer cell growth in an individual. The markers can be used as targets
CC in developing anti-cancer agents such as chemotherapeutic compounds. The
CC markers can also be used as targets in developing treatments for cancer,
CC particularly those cancers which display resistance to agents and exhibit
CC expression of the markers. The anticancer agents developed by the novel
CC method can be used to treat cancer. Probes based on the markers can be
CC used to detect transcripts or genomic sequences corresponding to the
CC disease and tumours (e.g. glioma). The present sequence is one of the
CC 1046 novel cancer cell markers
XX
SQ Sequence 530 BP; 89 A; 100 C; 106 G; 183 T; 0 U; 52 Other;
Query Match 56.2%; Score 303; DB 4; Length 530;
Best Local Similarity 88.2%; Pred. No. 4.4e-75;
Matches 321; Conservative 0; Mismatches 41; Indels 2; Gaps 1;

QY 178 AGTCATGAAGTGGAAACGACG--AACACCTGAAGAGGGGACACGACCACTCAACGTCAGG 235
Db 449 AGTATNAAGTGGAGCCCAACNACNCCCTGAANAAGGNAACCAACGCACTCAACGTTNAGG 390
QY 236 ATCTCTGACGCTGCTCAGGAGGAGGATGAGGAGGATCTGCGAGGTCAAGGCCGGAAGC 295
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Db 389 ATCTCTGNAGCTGCNCAGNAGGGANAGGATNAGGNGCAINTGCAGGTCAAGGCCGGAAGC 330
QY 296 CTGAAGCTGATAGCCAGGAAACAGGGTCAACCACAGACTGGGTGTGAGTGTGAAGATGGTC 355
|||||
Db 329 CTGAAGTGTATAGCCAGGAAACAGGGTCAACCACTGGGNGTNAAGTGTNAAGATGGTC 270
|||||
QY 356 CTGATGGCAGGAGGTGGACCCGCCAAATCCAGAGGAGGTGAAAACGCTTGAAGAAGGTG 415
|||||
Db 269 CTNATGGCAGNANATGGACCCNCCAAATCCAAAGNAGGTGAAAACNCCCTGAAANAAGGTG 210
|||||
QY 416 AAAAGCAATCACTGTTTAAAGAACACACAGCTTGAATGATGTCAGGCTGCTCTATGTTG 475
|||||
Db 209 AAAAGCAATCCCACTGTTTAAANANAGGNCGTTGAAATGATGACGGCTGCTCTATGTTG 150
|||||
QY 476 GAAATTTGTTTCATTAATAATTTCTCCCAATAAAGCTTTACAGCCTTTCTGCAAAAAA 535
|||||
Db 149 GAAATTTGTTTCATTAATAATTTCTCCCAATAAAGCTTTACAGCCTTTNNAAAAAA 90
|||||
QY 536 AAAA 539
Db 89 AAAA 86

RESULT 14
AAS60496/c
ID AAS60496 standard; cDNA; 365 BP.
XX
AC AAS60496;
XX
XX 29-JAN-2002 (first entry)
DT
XX
DE Human cancer agent-sensitive marker #227.
XX
XX Human; cancer cell marker; TAXOL; cytostatic; tumour; carcinoma;
KW squamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia;
KW lymphocytic leukaemia; lymphoma; plasmocytoma; reticulum cell sarcoma;
KW Hodgkin's disease; glioma; ss.
XX
XX Homo sapiens.
XX
XX WO200179556-A2.
XX
XX 25-OCT-2001.
XX
XX 13-APR-2001; 2001WO-US012132.
XX
XX 14-APR-2000; 2000US-0197538P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lillie J, Brown JL, Bolt A, Van Huffel C;
XX
XX WPI; 2001-602933/68.
XX
XX Novel nucleic acid, used as a marker to determine the effectiveness of
PT using TAXOL to treat cancer cell growth in individuals.
XX
XX Claim 1; Page 231; 527pp; English.
XX
XX The invention relates to 1046 novel nucleic acids which are used as
CC markers for determining the sensitivity of a cancer cell to the
CC anticancer agent TAXOL. Cancer cells can be treated with TAXOL when they
CC are shown to express one of the 242 sensitivity markers or the cells are
CC shown not to express one of the 804 resistance markers. The methods can
CC be used to determine the effectiveness of TAXOL in the treatment of
CC cancer cell growth in an individual. The markers can be used as targets
CC in developing anti-cancer agents such as chemotherapeutic compounds. The
CC markers can also be used as targets in developing treatments for cancer,
CC particularly those cancers which display resistance to agents and exhibit
CC expression of the markers. The anticancer agents developed by the novel
CC method can be used to treat cancer. Probes based on the markers can be
CC used to detect transcripts or genomic sequences corresponding to the
CC markers, in the identification of cells or tissues which mis-express the
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CC protein. Cancers which may be targeted include carcinoma (e.g. squamous  
CC cell carcinoma), sarcoma (e.g. fibrosarcoma) leukaemia (e.g. lymphocytic  
CC leukaemia), lymphoma, plasmocytoma, reticulum cell sarcoma, Hodgkin's  
CC disease and tumours (e.g. glioma). The present sequence is one of the  
XX 1046 novel cancer cell markers  
SQ Sequence 365 BP; 63 A; 86 C; 66 G; 150 T; 0 U; 0 Other;

Query Match 55.8%; Score 300.8; DB 4; Length 365;  
Best Local Similarity 96.2%; Pred. No. 1.6e-74;  
Matches 308; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
QY 220 GCAACTCAACGTCAGACTCCGACGCTGTCAGGAGGAGAGGATGAGGGACATCTGCA 279  
Db |||||  
365 GCAACTCAACGTCAGACTCCGACGCTGTCAGGAGGAGAGGATGAGGGACATCTGCA 306  
QY 280 GGTCAAGGGCCGAAAGCCTGAAAGCTGATAGCCACGAGGAGGATCAACACAGACTGGGT 339  
Db |||||  
305 GGTCAAGGGCCGAAAGCCTGAAAGCTGATAGCCACGAGGAGGATCAACACAGACTGGGT 246  
QY 340 GAGTGTGAAGATGCTCTGATGGGCGAGGAGTGGACCCGCAATTCAGAGAGGTGAAA 399  
Db |||||  
245 GAGTGTGAAGATGCTCTGATGGGCGAGGAGTGGACCCGCAATTCAGAGAGGTGAAA 186  
QY 400 ACGCCTGAAGAGGTGAAAAGCAATCACAGTGTGTTAAAAAGAGACACGTTGAAATGATGCA 459  
Db |||||  
185 ACGCCTGAAGAGGTGAAAAGCAATCTCAGTGTGTTAAAAAGGACGTTGAAATGATGCA 126  
QY 460 GGTGCTCCTATGTTGGAAAATTGTTCAATTAATAATTCCTCCCAATAAAGCTTTACAGCCTT 519  
Db |||||  
125 GGTGCTCCTATGTTGGAAAATTGTTCAATTAATAATTCCTCCCAATAAAGCTTTACAGCCTT 66  
QY 520 CTGCAAAAAAATAAAAAA 539  
Db 65 CTAAAAAATAAAAAA 46

## RESULT 15

ABZ19551/C  
ID ABZ19551 standard; cDNA; 277 BP.

XX AC ABZ19551;

XX DT 23-JAN-2003 (first entry)

XX DE Group III cDNA cancer related clone SEQ ID NO:1977.

XX KW Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;  
KW immune response; virology; immunology; microbiology; molecular biology;  
KW recombinant DNA technology; gene; ss.

XX OS Homo sapiens.

XX FN WO200278516-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US010421.

XX PR 30-MAR-2001; 2001US-0280255P.

XX PR 28-AUG-2001; 2001US-0315563P.

XX PR 09-JAN-2002; 2002US-0347313P.

XX PA (CORI-) CORIXA CORP.

XX PI Wang T, Wang S, Bangur CS, Gaiger A;

XX DR WPI; 2003-058387/05.

XX PT New immunogenic polynucleotides or polypeptides useful for diagnosing,  
PT preventing and treating cancer expressing CT or CP mRNA antigens, and in  
PT virology, immunology, microbiology, molecular biology and recombinant DNA  
PT techniques.

XX PS Claim 1; SEQ ID NO 1977; 207pp; English.

XX ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and  
CC ABP54446 to ABP54472 represent protein (II) sequences, from the present  
CC invention. (I) and (II) have cytostatic activity and can be used in gene  
CC therapy and vaccines. (I), (II), antibodies and compositions from the  
CC present invention are useful for diagnosing, preventing and treating  
CC cancer, which expresses CT or CP mRNA antigens. They are useful for  
CC stimulating immune response. They can also be useful in virology,  
CC immunology, microbiology, molecular biology and recombinant DNA  
CC techniques. N.B. The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 277 BP; 62 A; 79 C; 73 G; 63 T; 0 U; 0 Other;

Query Match 45.3%; Score 244; DB 7; Length 277;

Best Local Similarity 100.0%; Pred. No. 1.4e-59;

Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGGGAGCTGTGAGGAGTGTGTTGTTCTCGCTCGGACTCTTTTCTCTAC 60

Db |||||

244 GCCAGGGAGCTGTGAGGAGTGTGTTGTTCTCGCTCGGACTCTTTTCTCTAC 185

QY 61 TGAGATTTCATCTGTGTAATATGAGTTGGCGAGGAAGATCGACCTATTATGGCCTAGA 120

Db |||||

184 TGAGATTTCATCTGTGTAATATGAGTTGGCGAGGAAGATCGACCTATTATGGCCTAGA 125

QY 121 CCAAGGCGCTATGTACAGCCTCCTGAGTGATTGGGCTATGCGGCCGAGCAGTTCAGT 180

Db |||||

124 CCAAGGCGCTATGTACAGCCTCCTGAGTGATTGGGCTATGCGGCCGAGCAGTTCAGT 65

QY 181 GATGAAGTGGAAACGAGCAACACCTGAAAGAGGGGAAACGAGCAACTCAACGTCAGGATCCT 240

Db |||||

64 GATGAAGTGGAAACGAGCAACACCTGAAAGAGGGGAAACGAGCAACTCAACGTCAGGATCCT 5

QY 241 GCAG 244

Db |||||

4 GCAG 1

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Job time : 395 secs

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